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(FILE 'REGISTRY' ENTERED AT 08:37:37 ON 15 JUL 2001)

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- E PCAPGTFSNTTSSTDICRPHQIC/SQEP
- E PCAPGTFSNTTSSTDICRPHQICNVVALIPGNASMDAVCT/SQEP
- E TSTSPTRSMAPGAVHLP/SQEP
- E STSPTRSMAPGAVHLP/SQEP

No lits on closed sequences

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leader peptide [immu-conotoxin GIIIA antigen (clone PV1 24K antigen - Myco arylsulfatase A - convulsant peptide aspartylglycosamin paralytic peptide paralytic peptide substance P - rain
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trypsin (EC 3 4.21
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self-incompatibili
                                                         July 13, 2001, 17:15:46; Search time 12.7 Seconds (without alignments) 137.954 Million cell updates/sec
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T-cell receptor be
T-cell antigen rec
30K allergen - rye
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gene HEXA protein
LX-1 tumor antigen
homeodomain protei
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peptidylglycine mo
T-cell receptor be
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GenCore version 4.5 . Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                       219241 seqs, 76174552 residues
                                                                                                US-09-800-909-2_COPY_163_185
134
1 PCAPGTFSNTTSSTDICRPHQIC 23
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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B49048
S47381
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T-cell receptor al hemoglobin beta-2 collagen alpha 3(I alpha-conotoxin Phelothermine - Mex paralytic peptide paralytic peptide paralytic peptide tremerogen A-10 - bma protein - Clos R-phycoertyhrin ga 36k protein 3124 - T-cell receptor al lutropin beta chal vasotocin-associat T-cell receptor al Ig H chain V-D-J r	ALIGNMENTS	undent myosin light chain kinase (autophosphorylation sites) - us cuniculus (domestic rabbit) #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997 C.R.; Hsu, J.; Slaughter, C.A.; Stull, J.T. 6-6133, 1992 ryplation of skeletal muscle myosin light chain kinase. A42865; MUID:92329432 y veloc) ie: skeletal muscle ie: skeletal muscle irracted from NCBI backbone (NCBIP:109204)	re 31; DB 2; Length 20; d. No. 4.8e+02; Mismatches 9; Indels 0; Gaps 0;	eceptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen is: Homo sapiens (man) 23Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997 10n: B49048 M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O. Immunol. 22, 2413-2418, 1992 Limited heterogeneity of T cell receptor variable region gene usage in juven nnce number: A49048; MUID:92387250 10n: B49048 I: preliminary; not compared with conceptual translation ses: 1-18 csio> mental source: patient EV, IL-2R+ synovial T-cells sequence extracted from NCBI backbone (NCBIP:113264)	re 30; DB 2; Length 18; d. No. 66+02; Mismatches 4; Indels 0; Gaps 0;
PH0776 CA05305 CA05305 CA05305 CA05305 AA05305 AA05309 PH0799 PH0799 PH0782 PH0782 PH0782	ALIGN	vosin light che culus (domestic ce_revision 18 18u, J.; Slaug) 1992 n of skeletal n MUID:92329432 Aum NCBI backh	Score 3 Pred. N 1; Mism	region (CDR3 ju)) De_revision 18-Nu J.; Suleyman, 8 118, 1992 Lty of T cell rec MuID:92387250 compared with coi	Score 3 Pred. N 1; Mism
ппппппппппппппппппппппппппппппппппппппп		myosin iculus nce_rev nse_rev 1992 on of s ; MUID: MUID: from M	44 46 46 46 7	V region n) ce_revis: ce_revis: 1, J.; Su 418, 199; ity of T MUID:92: compared ent EV, from NCB	ar ar
41122330 		ent myosin cuniculus squence_re squence_re 5133, 1992 lation of lation of 2865; MUID in skeletal cted from	11arity 37.5%; Conservative NTTSSTDICR 18 :       QAKAQGDTCR 17	chain V regions (man) sequence_review (man) sequence_review (man) 1. 5 2413-2418, 19 249048; MUD:9 49048; MUD:9 into compare in patient EV, acted from NC coeptor	22.4%, larity 50.0%, Conservative
177.99 177.19 177.22 177.22 177.22 177.22 177.22 177.22 177.22		lin-dependent myos ar-1993 #sequence_ A42865 Moomaw, C.R.; Hsu 31, 6126-6133, 19 onumber: A42865; MU A42865 eliminary ype: protein al source: skeleta ence extracted fro	tch al Similarity 6; Conservat APGTESNTTSSTDICR     APGQADQAKAQGDICR	beta ci sapien 1994 #sy 1994 #sy 1904 #s eldsen-i . 22, 2 d heter d he	Similarity 5; Conserv
44400000000000000000000000000000000000		RESULT 1 44.2865 Ca2+/calmodulin-dependent myosi C;Species: Orytclagus cuniculu C;Date: 04-Mar-1993 #sequence_r C;Accession: 44.2865 R;Gao, Z.H.; Moomaw, C.R.; Hsu, Biochemistry 31, 6126-6133, 199 A;Title: Autophosphorylation of A;Reference number: 44.2865; MUI A;Accession: A4.2865; MUI A;Accession: A4.2865; MUI A;Accession: A4.2865; MUI A;Accession: A4.2865; MUI A;Accession: A1.2865; MUI A;Accession: A2.2865; MUI A;Accession: A2.	. R O	RESULT 2 B49048 T-cell receptor beta chain V regio C; Species: Homo sapiens (man) C; Date: 21-Jan-1994 #sequence_revi C; Accession: B49048 R; Sioud, M.; Kjeldsen-Kragh, J.; S Eur. J. Immunol. 22, 2413-2418, 19 A; Title: Limited heterogeneity of A; Reference number: A49048; MUID: 9 A; Accession: B49048 A; Status: preliminary; not compare A; Molecule type: mRNA A; Residues: 1-18 < SLO> A; Experimental source: patient EV, A; Note: sequence extracted from NC C; Keywords: T-cell receptor	al al
0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		ESULT 42865 a24-Ca 324-Ca 35Pec1a Date: Access	Query M Best Lo Matches Qy 3	RESULT BB904B BB904B C.Specie C.Chotes C.Chotes R.Sioud A.Fefere A.Access A.Status A.Molec A.Molec C.Kebec C.Kebec C.Kebec C.Keywon	Query Ma Best Loc Matches

2 CAPGTFSNTT 11

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C;Accession: A39269
R;Rosenbaum, L.C.; Neuwelt, E.A.; Van Tol, H.H.M.; Loh, Y.P.; Verbalis, J.G.; Hellstr Proc. Natl. Acad Sci. U.S.A. 87, 9928-9932, 1990
A;Title: Expression of neurophysin-related precursor in cell membranes of a small-cel A;Reference number: A39269; MUID:91088624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribegnan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
A; Title: Identification of eight homeobox-containing transcripts expressed during lar
                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C;Accession: I54351
R;Akli, S: Chomel, J.C.; Lacorte, J.M.; Bachner, L.; Poenaru, A.; Poenaru, L.
Hum. Mol. Genet. 2, 61-67, 1993
A;Title: Ten novel mutations in the HEXA gene in non-Jewish Tay-Sachs patients.
A;Reference number: I54351; MUID:93258352
A;Accession: I54351
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C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 05-Jan-1996
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C;Species: Haliotis rufescens (California red abalone)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
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ilarity 80.0%; Pred. No. 9.8e+02;
Conservative 0; Mismatches 1; Indels
                                                                 Indels
Pred. No. 7.7e+02;
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52.6%; Pred. No. 9.4e+02;
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                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
                                                                                                                                                                                                                                                                                                                                                 gene HEXA protein - human (fragment)
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A;Residues: 1-22 <ROS>
C;Superfamily: oxytocin-neurophysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase
                             38.5%;
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                                Best Local Similarity 38.5
Matches 5; Conservative
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                                                                                                                            3 APGTFSNTTSSTD
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Best Local Similarity
Matches 4; Conserv
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Matches 10; Conser
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A; Residues: 1-21 <RES>
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|PCGPG 16
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318292
30 Allergen - rye (fragment)
C;Species: Secale cereale (rye)
C;Species: Secale cereale (rye)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 07-May-1999
C;Accession: 538292
R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A;Title: Comparison of four grass pollen species concerning their allergens of grass grc
A;Reference number: 538288; MUID:94092339
                                                                                                                                                                                                              T-cell antigen receptor VJ junction beta chain - human (Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: Of-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (C.Accession: S47381 (C.Accession: S47381 (C.Accession: Britcher, P.J. (C.Accession: S47381 (C.Acc
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C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 21-Nov-1997
C;Accession: A6031.
R;Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.
Regul. Pept. 13, 94, 1986
A;Title: A truncated glucagon-like peptide I from torpedo pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:235698; NID:g527487; PIDN:CAA84767.1; PID:g527488
C;Keywords: T-cell receptor
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Pred. No. 7.3e+02;
); Mismatches 1;
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ilarity 83.3%;
Conservative
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A.Residues: 1-17 <CON>
C.Superfamily: glucagon
C.Keywords: duplication; pancreas
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Matches 6; Conservative
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                                ||||| : |
CAPGXYYGYT 16
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Best Local Similarity
Matches 5; Conserv
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7 PAAPGT 12
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Biochemistry 30, 6908-6916, 1991

A;Title: Tertiary structure of conotoxin GIIIA in aqueous solution.

A;Title: Tertiary structure of conotoxin GIIIA in aqueous solution.

A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR

R;Ott, K.H.; Becker, S.; Gordon, R.D.; Rueterjans, H.

FEBS Lett. 278, 160-166, 1991

A;Title: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geo

A;Reference number: A5888; MUD:9112275

A;Reference number: A5888; MUD:9112275

A;Reference number: A6888; MUD:9112256

A;Contents: annotation; conformation by (1)H-NMR

B;Wakamatsu, K.; Kohda, D.; Hatanaka, H.; Lancelin, J.M.; Ishida, Y.; Oya, M.; Nakamu

A;Title: Structure-activity relationships of mu-conotoxin GIIIA: structure determinat

A;Reference number: A4424; MUD:93112598

A;Contents: annotation; conformation by (1)H-NMR

C;Superfamily; mu-conotoxin

C;Superfamily; mu-conotoxyl end; hydroxyproline; myotoxin; sodium channel inhibitor

F;315,4-20,10-21/Disulfide bonds: #status experimental

F;17/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F;22/Modified site: amidated carboxyl end (Ala) #status experimental
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C; Species: Mycobacterium bovis
C; Species: Mycobacterium bovis
C; Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Jun-1993
C; Accession: B60278
R; Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A; Title: Purification and characterization of major antigens from a Mycobacterium bov A; Reference number: A60278; MUID:91147217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax
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C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Sep-1997
C;Accession: JN0263; S21344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Biochem. Biophys. Res. Commun. 184, 668-672, 1992
A; Title: Molecular cloning and serological characterization of
A; Reference number: JN0263; MUID:92246949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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A,Molacule type: DNA
A,Residues: 1-15
A,Cross-references: GB:X53681; NID:g10084; PID:g10085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 1; I
Pred. No. 1.8e+03;
2; Mismatches 2;
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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54.5%;
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Best Local Similarity
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A.Residues: 1-22 <SAT>
R.Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydld
J. Blol. Chem. 260, 9280-9288, 1985
A.Title: Conus geographus toxins that discriminate between neuronal and muscle sodium ch
A.Reference number: A23579; MUID:85261316
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R;Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
R;Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
A;Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins from A;Reference number: A91309; MUID:83210170
A;Accession: A01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Vibrio sp.
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Accession: T48881
R; Xu, Y; Zhang, Y; Liang, Z.Y.; Van de Casteele, M.; Legrain, C.; Glansdorff, N.
Microbiology 144, 1435-1441, 1998
A; Title: Aspartate carbamoyltransferase from a psychrophilic deep-sea bacterium, Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1-22 <CRU>
R; Kohda, D.; Lancelin, J.M.; Inagaki, F.; Wakamatsu, K.
submitted to the Brookhaven Protein Data Bank, December 1992
A; Reference number: A51994; PDB:17CG
A; Contents: annotation; conformation by (1)H-NMR, residues 1-22
R; Lancelin, J.M.; Kohda, D.; Tate, S.I.; Yanagawa, Y.; Abe, T.; Satake, M.; Inagaki, F.
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MXKN1
mu-conotoxin GIIIA [validated] - cone shell (Conus geographus)
N.Alternate names: geographutoxin I (GTX I); myotoxin I
C;Species: Conus geographus (geography cone)
C;Species: 14-Nov-1993 #sequence_revision 14-Nov-1993 #text_change 15-Sep-2000
   A;Reference number: S60564; MUD:93372986
A;Accession: S60565
A;Accession: S60565
A;Cross-references: EMBL:X79372; NID:9495110; PIDN:CAA55917.1; PID:9495111
C;Genetics: A;Gene: hrox3
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                       20.9%; Score 28; DB 2; I 57.1%; Pred. No. 1.4e+03; ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 2; Pred. No. 1.7e+03; 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: 224845
A;Accession: T48881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-20 <XUY>
A;Cross-references: EMBL:Y09786; PIDN:CAA70922.1
A;Experimental source: strain 2693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leader peptide [imported] - Vibrio sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.1%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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7 SSLSSFKLVRPH 18
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Best Local Similarity
Matches 4; Conserv
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5 LCRPRRI 11
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Gaps

7;

Length 22; 4; Indels

Score 25.5; DB 2; Pred. No. 2.9e+03; ); Mismatches 4;

A; Residues: 1-22 <RES>

38.5%;

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A;Cross-references: EMBL:X73071; NID:g312227; PIDN:CAA51529.1; PID:g312228 C;Genetics:
A;Gene: AGU
                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: July 13, 2001, 17:17:28
Job time: 102 sec
                                                                                                                                                      19.0%;
38.9%;
                                                                                                                                                                                                                                                                                           5 TFSRRVS-----HHIC 15
                                                                                                                                                                                                                                                            TFSNTTSSTDICRPHQIC 23
                                                                                                                               Ouery Match
Best Local Similarity 38.55
Best Local 7; Conservative
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                                                                                                                                                                                                                                                 arylsulfatase A - human (fragment)
C; Species: Homo sapiens (man)
C; Stati (15428)
C; Accession: 154283
R; Regis, S.; Carrozzo, R.; Filocamo, M.; Serra, G.; Mastropaolo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995
A; Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infant A; Reference number: 154283; MUID:95362256
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aspartylglycosaminuria - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Date: 137144
R;Park, H; Vettese, M.B.; Fensom, A.H.; Fisher, K.J.; Aronson, N.N.
B;Dachen, J. 290, 735-741, 1993
A;Title: Characterization of three alleles causing aspartylglycosaminuria: two from a Br A;Reference number: 137144
A;Status: perliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
A59048
convulsant peptide - cone shell (Conus textile)
C;Species: Conus textile (cloth-of-gold cone)
C;Species: Conus textile (cloth-of-gold cone)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: A59048
R;Cruz, L.J.; Ramilo, C.A.; Corpuz, G.P.; Olivera, B.M.
Biol. Bull. 183, 159-164, 1992
A;Title: Conus peptides: phylogenetic range of biological activity.
A;Reference number: A59048
A;Accession: A59048
A;Accession: A59048
A;Residues: 1-23 <CRUD
C;Keywords: anidated carboxyl end; neurotoxin; venom
E;23/Modified site: amidated carboxyl end (Pro) #status predicted
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                               Gaps
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                            0;
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  Pred. No. 1.9e+03;
1; Mismatches 7; Indels
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Matches 5; Conservative
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July 13, 2001, 17:17:11; Search time 9.94 Seconds (without alignments) 79.263 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-800-909-2\_COPY\_163\_185 134 1 PCAPGTFSNTTSSTDICRPHQIC 23 Title: Perfect score:

Sequence:

93435 seqs, 34255486 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1257 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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SUMMARIES	ΙD	CXM1_CONGE	AFP2_BRANA	CP23_SPOER	PAP2_SPOEX	PAP3_SPOEX	TKNA_ONCMY	CXM2_CONGE	CXM3_CONGE	LANM_STRMU	HBB2_UROHA	DCMM_PSECA	CXAB_CONPE	HELT_HELHO	PAP1_HELVI	PAP2_HELVI	TA10_TREME	C1QA_RAT	PAP2_MANSE	JHBP_BOMMO	PAP1_SPOEX	CXAA_CONPE	RS11_SALTY	NUO3_SOLTU	CXA1_CONER	PSBH_SYNVU	SETB_SALTY	TX12_TRIWA	MIFH_TRISP	UCRQ_EQUAR	MCT3_MOUSE	RL5_HALHA	DCMM_PSECH	PAP1_MANSE
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	ENTS	22 AA.		u		B.M., Zeikus R.D., Kerr L., discriminate between neurona		PubMed-6852238; H., Ohizumi Y., Kobayashi J., Hirata Y equences of homologous hydroxyproline-c	geographus venom	Kobayashi J., Ohizumi	<u>α</u>			snails.";		Rueterjans H.; GIIIA analysed by		F ode V strangerev	in aqueous	MEMBRANE
CXA1_CONST LMA1_LOCMI CXA1_CONE HS11_PINPE RKGG_CARCR UREZ_MORNO UREZ_MORNO CXA2_CONST LPRM_STAAU SODF_PASTI FEDB_AMYME	ALIGNMENT	;	nce up ation	stropo ; Con		; cri	5).	; , Kob? ologo:	Conus	; Kobay	toxin		 	nus sı 988).		xin G		, F		
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		ONGE.	-1986 -1986 -1995 OTOXIN	geograpota ota; M tropod axID=6	CE. E-8526	ami D. geogr sodiu	l. Che	NCE. NE=8321 S., Nakamino a	ins fr ett. 1	IDE BO E=9024 Y., S.	shi Y. fide p geogra	ett. 2	E-8902	de tox Rev. B	URE BY E=9112	-H., B	ce geor	URE BY E=9129	i F.;	mistry
333 333 444 5433 5433 5433 5433 5433 54		CONGE	21-JUL 21-JUL 21-JUL 01-FEB MU-CON	Conus Eukary Neogas NCBI_T	11   SEQUENCE. MEDLINE-85261316;	Cruz L.J., Gray W.R Yoshikami D., Moczy "Conus geographus t muscle sodium chann	J. Bio.	SEQUENCE. MEDLINE=83210170; E Sato S., Nakamura F "The amino acid sec	myotoxins from the FEBS Lett. 155:277	DISULFIDE BONDS. MEDLINE=90249506; I	Simonishi Y.; "Disulfide pairings i Conus geographus.";	FEBS L	MEDLING Gray W	pti u.	[5] STRUCTI MEDLIN	Ott KH., Becker S Solution structure	distance geometry calculations."; FEBS Lett. 278:160-166(1991).	STRUCTURE BY NMR. MEDLINE-91299744; Pubn	Inagak "Terti	Bioche -!- FU
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P30256;
                                                                                                         CP23_SPOER
P56683;
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"A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae species.";
FEBS Lett. 316:233-240(1993).
-i- FUNCTION: POSSESSES ANTIFUNGAL ACTIVITY SENSITIVE TO INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus (Rape).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnorliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicales; Brassicales; Rosidae; eurosids II;
CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                    PDB; 1TCH; 31-JAN-94.
PDB; 1TCJ; 31-JAN-94.
PDB; 1TCK; 31-JAN-94.
Sodium channel inhibitor; Hydroxylation; Amidation; Venom; 3D-structure.
3 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 1; Length 22;
Pred. No. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: FORMS OLIGOMERS IN ITS NATIVE STATE.

-!- SIMILARITY: BELONGS TO THE GAMMA-PUROTHIONIN FAMILY.

PIR; S28992; 238992.

HSSP; P30231; IAXJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
01-FBE-1994 (Rel. 28, Last annotation update)
CYSTEINE-RICH ANTIFUNGAL PROTEIN 2 (AFP2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                          F6CB02ADB359813C CRC64;
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Pred. No. 5.2e+02;
1; Mismatches 6;
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HYDROXYLATION.
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                                                                                                                                                                                                                                                                                                                                             AMIDATION
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28.6%;
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2467 MW;
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Best Local Similarity 28.6
Matches 4 4; Conservative
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                                     A01786; MXKN1.
A23579; A23579.
1TCG; 31-JAN-94.
1TCH; 31-JAN-94.
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23 AA;
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15 CKPQRCC 21
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J. Biol. Chem. 266:12873
-!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
PIR, D39855; D39855.
                                                                                                                                                                                                                                                                                                                                                                                      Peptides 20:53-61(1999).
-!- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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UENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;
                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pterygota: Neoptera: Endopterygota: Lepidoptera; Glossata: Ditrysia;
Noctuoidea: Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=7107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
                                                                                                                                                                                                                                                                                          Furuya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H., Shabanowitz J., Hunt D.F., Schooley D.A.; "A cardioactive peptide from the southern armyworm, Spodoptera eridania.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spodoptera exigua (Beet armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 23;
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0A96CB4600855AE0 CRC64;
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Pred. No. 8.5e+02;
2; Mismatches 7;
                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CARDIOACTIVE PEPTIDE CAP23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
23 AA.
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                                                                                                                               Spodoptera eridania (Southern armyworm).
                                                                                                                                                                                                                                                                                   MEDLINE=99196260; PubMed=10098624;
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MEDLINE-91302298; PubMed-2071576;
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33.3%;
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2477 MW;
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7 CTPG-YQRTADGR--CKP 21
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3 RPHQ 6
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-I-FUNCTION: CAUGES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-I-SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
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"Substance-P-related and neurokinin-A-related peptides from the brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropòda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
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Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
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0A96CB5EB7D55AE0 CRC64;
                                                   Score 25.5; DB 1;
Pred. No. 8.5e+02;
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01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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01-APR-1993 (Rel. 25, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
PARALYTIC PEPTIDE III (PP III).
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MEDLINE-92298992; PubMed-1376687;
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33.3%;
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2505 MW;
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                                             Query Match
Best Local Similarity
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23 AA;
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P30257;
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DISULFID
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PAP3_SPOEX
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AC P3025_SI
AC P3025_SI
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TKNA_ONCMY
AC P28499;
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Eur. J. Biochem. 206:659-664(1992).
--- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH.EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=96280640; PubMed=8688418;
Hill J.M., Alewood P.F., Craik D.J.;
Hill J.M., Alewood P.F., Craik D.J.;
"Three-dimensional solution structure of mu-conotoxin GIIIB, a specific blocker of skeletal muscle sodium channels.";
Blochemistry 35:8824-8835(1996).
-1- FUNCTION: MU-CONOTOXINS 'ACT ON MUSCLE MEMBRANES. THEY BLOCK MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
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Cruz L.J., Gray W.R., Olivera B.M., Zeikus R.D., Kerr L.,
Yoshikami D., Moczydlowski E.;
"Conus geographus toxing that discriminate between neuronal and
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Usukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6491;
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Sodium channel inhibitor; Hydroxylation; Amidation; Venom;
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Pred. No. 4.7e+02;
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PIR; S23307; S23308.
PIR; S23308; S23308.
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21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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100.0%; Pred. No.
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"Peptide toxins from venomous Conus
Annu. Rev. Biochem. 57:665-700(1988)
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J. Biol. Chem. 260:9280-9288(1985).
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PIR; B23579; B23579.
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Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Biochem. 5:665-700(1988).
-i- FUNCTION: MU-CONOTOXINS ACT ON MUSCLE MEMBRANES. THEY BLOCK
MUSCLE CONTRACTION BY BINDING TO THE VOLTAGE-ACTIVATED SODIUM
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Usukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6491;
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DISULEID 3 15 BY SIMILARITY.
DISULEID 4 20 BY SIMILARITY.
DISULEID 10 21 BY SIMILARITY.
MOD_RES 6 6 HYDROXYLATION.
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Yoshikami D., Moczydlowski E.;
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                                                                              Length 22;
                                                                                               4; Indels
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                                            AMIDATION.
F50402BA93199E01 CRC64;
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F50402BA92A9813C CRC64;
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Pred. No. 9.5e+02;
L; Mismatches 4;
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01-NOV-1988 (Rel. 09, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
MU-CONOTOXIN GIIIC.
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MEDLINE-85261316; PubMed-2410412;
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PIR; C23579; C23579.
HSSP; P01524; 1GIB.
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Best Local Similarity
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ID LANM_ST
AC P80666;
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ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF
LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL
CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NAY-1991 (Rel. 18, Last annotation update)
HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
Uromastyx hardwickii (Indian spiny-tailed lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE PORES.
-!- MASS SPECTROMETRY: MW-2270.29; MW_ERR-0.21; METHOD-ELECTROSPRAY.
-!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
InterPro; IPR001049; -.
Pfam; PF02052; Gallidermin; 1.
PRINTS; PR00323; GALLIDERMIN.
                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                Mota-Meira M., Lacroix C., Lapointe G., Lavoie M.C.; "Purification and structure of mutacin B-Ny266: a new lantibiotic produced by Streptococcus mutans."; FEBS Lett. 410:275-279(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 22;
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FEBS Lett. 162:290-295(1983).

PIR; A05305; A05305.

InterPro; IPR000971; -,

PROSITE; PS01033; GLOBIN; PARTIAL.

Heme; Oxygen transport; Respiratory protein; Erythrocyte.

NON_TER 1 1
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Pred. No. 1.1e+03;
; Mismatches 8;
                            Last sequence update)
Last annotation update)
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                                                     01-OCT-2000 (Rel. 40, Last an
LANTIBIOTIC MUTACIN B-NY266.
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01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 01-OCT-2000 (Rel. 40,
                                                                                                      Streptococcus mutans.
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=8552;
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ID HELT_H
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01-FEB-1991 (Rel. 17, Last sequence update)
01-UNN-1994 (Rel. 29, Last annotation update)
CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] MEDIUM CHAIN (EC 1.2.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kraut M., Hugendleck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- CATALYTITA CATIVITY: CO + H(2)O + FERROCYTOCHROME B-561 = CO(2)
2 H(+) + FERRICYTOCHROME B-561.
-!- COFACTOR: MOLYBDENUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas carboxydovorans.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizoblum group; Oligotropha.
NCBI_TaxID=40137;
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Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
Spira M.E., Zlotkin E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mollusc-specific alpha-conotoxins block Aplygia neuronal
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Pred. No. 1.1e+03;
1; Mismatches 4; Indels
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Neogastropoda; Conoidea; Conidae; Conus.
NCBL_TaxID=37335;
                                                                                                                   17.9%; Score 24; DB 1; Length 19; 41.7%; Pred. No. 1.1e+03;
                                                                                                                                                                           5; Indels
     19
1914 MW; C40AD8EA30019057 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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36.8%;
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NON_TER 15 15
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Best Local Similarity 36.0.
For 7; Conservative
                                                                                                                                                                              Conservative
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19 AA;
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P19920:
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P50985;
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OC CONUS
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DCMM_PSECA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1AKG; 20-MAY-98.
Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
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"Isolation and characterization of helothermine, a novel toxin from Heloderma horridum (Mexican beaded lizard) venom.";
Toxicon 28:299-309(1990).
-!- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT MIGHT BE A HYPOTHERMIC TOXIN.
-!- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA AND A D OF 68:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97444322; PubMed-9299951;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
Comparison with alpha-conotoxins PnIA and GI.";
Biochemistry 36:11323-11330(1997).

BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
11-NOV-1995 (Rel. 32, Last annotation update)
HELOTHERMINE (FRAGMENT).
Heloderma horridum horridum (Mexican beaded lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                             SULFATATION OF TYR-15.
MEDLINE-99242956; PubMed-10226369;
Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
Baldwin M.A., Burlingame A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23.5; DB 1; Length 16; Pred. No. 1.1e+03; 1; Mismatches 3; Indels
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05310FF95ED86AF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                   spectrometry.";
J. Mass Spectrom. 34:447-454(1999).
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MEDLINE=90260878; Pubmed=1693019;
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DISULFID 2 8
DISULFID 3 16
DISULFED 15 15
MOD_RES 16 16 AMID
SEQUENCE 16 AA; 1643 MW; 0531
acetylcholine receptors.";
Biochemistry 33:9523-9529(1994).
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35.3%;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L., Quistad G.B., "Isolation and identification of paralytic peptides from hemolymph of the lepidopteran insects Manduca sexta, Spodoptera exigua, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heliothis virescens.";
J. Biol. Chem. 266:12873-12877(1991).
-!- FUNCTION: CAUSES RAPID, RICID PARALYSIS WHEN INJECTED INTO
-!- FUNCTION: CAUSES RAPID, RICID PARALYSIS WHEN INJECTED INTO
-!- EPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
-!- SIMILARITY: BELONGS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
PIR; F39855; F39855.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1999 (Rel. 38, Last annotation update)
PARALYTIC PEPTIDE II (PP II).
Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryotta; Metazoa Arthropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Heliothinae; Heliothis.
Not_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUR-Hemolymph;
MEDLINE-191302298; PubMed-2071576;
Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad (.B.;
                                                                                                                                 ä
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                                                                          Length 20;
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                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
91D62B36F7B4F940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
2236CB436D655AFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.5; DB 1;
Pred. No. 1.6e+03;
2: Mismatches 7;
                                                                          Score 23.5; DB 1;
Pred. No. 1.4e+03;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Noctuid moth) (Owlet moth)
                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PARALYTIC PEPTIDE I (PP I).
Heliothis virescens (Noctuid moth) (Owlet moth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AA.
                                                                                                                                                                                                                                                                                                                                                            23 AA
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hemolymph;
MEDLINE=91302298; PubMed=2071576;
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2524 MW;
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33.3%;
                                                                          17.5%;
41.2%;
2156 MW;
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                                                                                                                                                                           1 PCAPGTF-SNTTSSTDI 16
                                                                                                                                                                                                              4 PKLPGLMTSNPDQQTEI 20
                                                                          Query Match 17.5
Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity
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AA;
  AA;
20
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P30251;
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P30252;
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SEQUENCE
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PAP1_HELVI
DD PAP1_HI
DD PAP1_HI
DD 01-APR
DT 
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PAP2_HELVI
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"Isolation and identification of paralytic peptides from hemolymph of the lepidopteran insects Manduca sexta, Spodoptera exigua, and Heliothis Virescens.";
J. Blod. Chem. 266:12873-12877(1991).
-!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYWPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
PIR; G39855; G39855.
                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                    Score 23.5; DB 1; Length 2
Pred. No. 1.6e+03;
2; Mismatches 7; Indels
                                                                                                                                                                                                                 2236CB5D6C855AFA CRC64;
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                                                                                                                                                                                                                                                                                         17.5%;
                                                                                                                                                                                                                    2508 MW;
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                                                                                                                                                                                                                                                                                                                                                                                    CAPGTFSNTTSSTDICRP 19
                                                                                                                                                                                                                                                                                                                                        6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                Hemolymph.
SEQUENCE
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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099ugnB homo sapien
098923 brassica ol
07886 human immun
078507 human immun
078509 human immun
078509 human immun
0998fB glomus moss
099046 sapien
069142 streptococc
                                                                       P97944 mus musculu
Q9twc6 dirofilaria
Q9ugn8 homo sapien
Q9s923 brassica ol
                                                                                                                                                                                                    O9pru6 gallus gall
O9pru7 gallus gall
O85719 recovirus sp
Q78345 human immun
Q9qvd6 rattus sp.
Q9utt6 schizosacch
Q9ur51 filobasidie
P90716 beroe ovata
                                                                                                                                                                        Q9s8b9 lupinus alb
Q9uc48 homo sapien
Q9npq7 homo sapien
                                   Q9qex5 human 1mmun
                                            099ex4 human 1mmun
013726 homo sapien
09s922 brassica ol
                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
01-GODENDROCYTE-SPECIFIC UDP-GAALACYOSE:CERAMIDE GALACTOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                            "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLQSRSD (FLORIDA LOCAL CONTROL 01), PARTIAL ENV CDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.6%; Score 33; DB 11; Length 15
66.7%; Pred. No. 1.2e+02;
.ive 1; Mismatches 2; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA.
                                                                                                                                                                                                                                                           ALIGNMENTS
                09UR51
P90716
09QEX5
                                                                       P97944
Q9TWC6
Q9C918
Q9C918
Q78486
Q78507
Q78509
Q78509
Q978F8
Q9978F8
Q9978F8
Q9978F8
Q9978F8
Q9978F8
Q9978F8
                                            090EX4
013726
09S922
                                                                                                                                                                                                              Q9PRU7
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE-96085162; PubMed-8521863;
Schulte S., Stoffel W.;
Ouery Match 24.6
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGION (FRAGMENT).
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2 PGIFXSTTS 10
(FRAGMENT).
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Q9QUY5
Q9QUY5;
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Q78505;
RESULT
Q78505
                                                                                                                                                                                                                                                                                               Q9QUY5
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078378 human immun
078379 human immun
078380 human immun
025086 herdmania m
025134 hallotis ru
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086611 human immun
026159 plasmodium
09trh7 canis famil
09s885 lupinus alb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9quy5 rattus sp. 078505 human immun Q78381 human immun Q9qex3 human immun Q16017 homo sapien
                                                                       (without alignments)
145.599 Million cell updates/sec
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P96173 vibrio sp.
Q9twr5 phoneutria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                            July 13, 2001, 17:16:56; Search time 20.9 Seconds
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                425026 segs, 132305027 residues
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                                                                                                                  PCAPGTFSNTTSSTDICRPHQIC 23
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Maximum .Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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078378
078327-
078380
025086
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Q78505
Q78381
Q9QEX3
Q16017
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P96173
Q9TWR5
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Q26159
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Q9S885
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sp_invertebrate:*
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sp_rodent:*
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Match
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Gaps

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Result

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                            SEQUENCE FROM N.A.
Lin H.J., Siwak E.B., Hollinger F.B.;
Lin H.J., Siwak E.B., Hollinger F.B.;
Mutation rate of human immunodeficiency virus type 1 genomic 1 deduced from long term culture of its biological clones.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF178667; AAF04373.1;
Envelope protein.
NON_TER
1
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NON_TER
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93258352; PubMed-8490625;
Akli S., Chomel J.C., Lacorte J.M., Bachner L., Poenaru A.,
Poenaru L.;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 4; Lengtn 21;
Pred. No. 7.18+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
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                                                                                                                                                                                                                                                                                                                                                            E17BAC9DD31D9910 CRC64;
                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HEXA POTEIN (FRAGMENT).
                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 14;
Pred. No. 6.1e+02;
2; Mismatches 6;
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 18 AA
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 PRT;
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52.6%; Pred
0; }
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EMBL, S61298; AAD13927.1; --
HSSP; P06865; 1QBC.
                                                                                                                                                                                                                                                                                                                                                                                                              21.6%;
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 PRELIMINARY;
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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                    Q9QEX3;
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Q78323
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AC Q7
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01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-NOY-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5F (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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EMBL; M92126; AAA44496.1; -.

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NON_TER 17 17

NON_TER 17 17

SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;
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40.0%; Pred. No. 4.8e+02;
Live 3; Mismatches 6; Indels
                                                                                     Zhang L.Q., Leigh-Brown A.J.; Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
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Zhang L.Q., Leigh-Brown A.J.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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20 AA; 2049 MW; F44F963A48755A07 CRC64;
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 45.5
Matches 5; Conservative
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5A (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
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Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
EMBL; M92123; AAA44493.1;
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01-NQV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPAR5A (FLORIDA PATIENT A), PARTIAL ENV CDS, V5
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Pred. No. 8.3e+02;
2; Mismatches 4; Indels
                                                                                                   SEQUENCE FROM N.A. Zhang L.Q., Leigh-Brown A.J.; Zhang L.Q., Leigh-Brown A.J.; Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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MEDLINE-92271245; Pubmed-1589796;
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Best Local Similarity 45.5
Matches 5; Conservative
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NNTNETETFRP 13
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPARSD (FLORIDA PATIENT A), PARTIAL ENV CDS, V5 REGION
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBRSE (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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EMBL: M92125; AAA44495.1; -
NON_TER 1 1
SEQUENCE 17 AA: 1651 MW; 34757BBFD12CA370 CRC64;
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"Molecular epidemiology of HIV transmission in a dental practice.";
Science 256:1165-1171(1992).
EMBL; M92112; AA44468.1; -.
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SEQUENCE 17 AA; 1651 MW; 34757BBFD12CA370 CRC64;
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Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
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17 AA; 1651 MW; 34757BBFD12CA370 CRC64;
                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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3 NNTNGTETFRP 13
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"Identification of eight homeobox-containing transcripts expressed during larval development and at metamorphosis in the gastropod mollusc Hallotis rufescens.";
Mol. Mar. Biol. Biotechnol. 2:1-9(1993).
EMBL: X79372, CAA55917.1;
HSSP: P(22833: 9ANT.
InterPro; IPR001356;
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Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
NCBI_TaxID=6454;
20.9%; Score 28; DB 14; Length 17; 45.5%; Pred. No. 8.3e+02;
                                             4; Indels
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Pred. No. 1e+03;
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Kennett C.V.D.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U09939; AAA18629.1; --
HSSP; P02833; 9ANT.
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
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Stolidobranchia; Pyuridae; Herdmania.
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01-NOV-1996 (TrEMBLrel. 01, Last sequency
01-OCT-2000 (TrEMBLrel. 15, Last annotat.
CLONE AHOX4 HOMEOBOX PROTEIN (FRAGMENT).
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MEDLINE=93372986; PubMed=7689904;
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57.1%;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRAL SAMPLE FLPBR5C (FLORIDA PATIENT B), PARTIAL ENV CDS, V5 REGION
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MEDLINE-92271245; PubMed-1589796;
Ou C.Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,
Corder B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
Curran J.W., Jaffe H.W.;
"Molecular epidemiology of HIV transmission in a dental practice.";
Ecience 256:1165-1171(1992).
EMBL; M92124; AAA44494.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=79682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 14; Length 17; Pred. No. 1.2e+03;
                                                                                                                                          Score 28; DB 5; Length 23;
Pred. No. 1.1e+03;
2; Mismatches 1; Indels
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Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                           CC387AE7BDA6C44D CRC64;
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NON_TER 17 17
SEQUENCE 17 AA; 1652 MW; 34757BBFD1240170 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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MEDLINE=98274751; PubMed=9611817;
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45.5%;
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57.1%;
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Pfam; PF00046; homeobox; 1.

NON_TER 1 1

NON_TER 23 23

SEQUENCE 23 AA; 2793 MW;
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Best Local Similarity
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Pfam; PF00046; homeobox;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Morone saxatilis (Striped bass).
Morone saxatilis (Striped bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostel; Euteleostei; Neoteleostei;
Moronidae; Morone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olymar.2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PNV2 TOXIN (FRAGMENT).
Eukaryota: Matazoa: Arthropoda: Chelicerata: Arachida: Araneae: Araneomorphae: Entelegynae: Lycosoidea: Ctenidae: Phoneutria.
bacterium, Vibrio strain 2693: properties of the enzyme, genetic organization and synthesis in Escherichia coli."; Microbiology 144.1435-144(11998).
EMBL; Y09786; CAA-022.1; -. SEQUENCE 20 AA; 2241 MW; 35C31F588FBB5D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Debto A.C., Novello J.C., Marangoni S., Antunes E., Giglio J.R., Oliveira B., de Nucci G.; Marangoni S., Antunes E., Giglio J.R., Oliveira B., de Nucci G.;
"Identification of a new vascular smooth muscle contracting polypeptide in Phoneutria nigriventer spider venom.";
Biochem. Pharmacol. 46.1092-1095(1993).
SEQUENCE 20 AA; 2176 MW; F28C3D81D983BCA5 CRC64;
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BDDLINE-SEQUEDING,
BAVELINE-SO005122; PubMed-7921046;
Pavell A.M., Stellwag E.J.;
Survey of Hox-like genes in the teleost Morone saxatilis:
implications for evolution of the Hox gene family.";
MOI. Mar. Biol. Biotechnol. 3:149-157(1994).
HSSP: P02833; 9ANT.
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KW Homeobox; Nuclear protein; DNA-binding.
FT NON_TER 1 2 2
SQ SEQUENCE 22 AA; 2703 MW; AE4485CB7FF7CFID CRC64;
SQ SEQUENCE 22 AA; 2703 MW; AE4485CB7FF7CFID CRC64;
Ouery Match
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps
Oy 16 ICRPHQI 22
III ::
Db 2 LCRPRRV 8
Search completed: July 13, 2001, 17:19:39
Job time: 163 sec
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July 13, 2001, 17:14:30 ; Search time 17.98 Seconds (without alignments) 77.550 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Costant and variab	P. pastoris lysyl	P. pastoris lysyl	Yada homologous pe	Human secreted pro	Hepatitis B surfac	Human APC protein	Human presentlin I	Dextranase N-termi	Sequence of immuno	MSF 1-alpha peptid
	ID	AAW95323	AAY51961	AAY51973	AAB51542	AAW73416	AAW65481	AAB23019	AAY20893	AAR75932	AAP50661	AAY28912
	DB	20	21	21	21	20	19	21	19	16	9	20
	Ouery Match Length DB ID	17	17	17	22	23	23	20	15	16	23	23
dР	Query Match	34.3	30.6	30.6	27.6	27.6	25.7	25.0	24.6	24.6	24.3	24.3
	Score	46	41	41	37	37	34.5	33.5	33	33	32.5	32.5
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Human ATM gene pro ATM epitope #1. H Pharmaceutically a Human umbilical co Peptide #19 for ep Antigenic peptide Human delta3 fragm TGF beta 2 mutant Erythropoletin rec Fibronectin-like s Fibronectin-like s Fibronectin-derive Immunopeptide deri Hepatitis C virus HCV E2 peptide E2- N terminal sequenc Sequence encoded b Conserved sequenc Sequence Erythropoletin rec Erythropo	W	of C. psitacci CPS92-106. body phase; replicating; probenicid; nfection; diagnostic; assay; MOMP; une; inflammatory; porphyria;
AAW07656 AAW31164 AAW33126 AAW33126 AAW14391 AAW165710 AAW65710 AAW65710 AAW65170 AAR1600 AAR1600 AAR1600 AAR1600 AAR1600 AAR10375 AAR161762 AAR16	AAW51947 AAY09379 ALIGNMENT	7 AA. equence mentary ponse; 1 autoimm
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                                                                                                                                                                                                  The invention relates to the diagnosis and management of infections by chlamydia species. The invention provides a composition that comprises at least two agents, where each of the agents is effective against a different phase of the chlamydial life cycle. The agents are selected from: (a) agents targetted against cryptic phase of chlamydial life cycle; (b) agents targetted against replicating phase of chlamydial life cycle; (c) agents targetted against replicating phase of chlamydial life cycle; (d) probenicid, and (e) antiporphyric acid. The composition is used to elicit a protective immune response to Chlamydia infection in an animal or human and is applied until the animal or human tests negative for Chlamydia infection. It is also used to treat biological material infected with Chlamydial phase, are used to diagnose disease, against recombinant major outer membrane protein (MOMP), and for DNA, amplification assays for chlamydial genes, are used to diagnose disease, e.g. autoimmune disease, an inflammatory disease or a disease that corcurs in an immuno-compromised individual, associated with Chlamydia infection. The kits are used to adetect chlamydial elementary bodies in a patient. The treatment reduces the accellular load of infectious Ebstein Barr virus. The method is also used to treat porphyria, by reducing the number of elementary bodies and applying a drug, e.g. cimetidine, and antioxidants, to reduce the adverse effects associated with porphyria. Sequences AMM95323 represent constant and cimetidine, are decomed and applying a species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lysys oxidase; lipoxygenase; protein disulfide isomerase; phenol oxidase; peroxidase; protein disulfide reductase; tyrosine oxidase; fodder; sulfhydryl oxidase; food additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                     Composition with two agents effective against different stages of chlamyddal life cycle : comprises agent targetted against cryptic phase, against elementary body phase, against replicating phase, probenicid and antiporphyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%; Score 46; DB 20; Length 17; 64.3%; Pred. No. 3.9; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. pastoris lysyl oxidase peptide fragment #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY51961 standard; peptide; 17 AA.
                                                                                                                                                                            Claim 4; Fig 3; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98DE-1040069
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                                 Stratton CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 64.3
Matches 9; Conservative
(UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CAPGIFSNITSSID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 casgtasnttvaad 14
                                                              WPI; 1999-059653/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pichia pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE19840069-A1
                               Mitchell WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY51961
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This invention describes a novel method to manufacture a preparation of an active substance, where the active substance is surrounded by at least one layer consisting of a protein that is cross-linked by an enzyme chosen from the group of lipoxygenase, protein disulfide isomerase, phenol oxidase and peroxidase, lysyl oxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases. Enzymes chosen from lipoxygenase, protein disulfide isomerase, phenol oxidase and peroxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidase, especially lysyl oxidase are useful for formulation of preparations of active substances. The method of the invention is used for manufacturing preparations of active substances. The preparations are useful as food additives or fodder or as paramaceuticals. AAYS1961-Y31962 represent fragments of the Pichia formatics lysyl oxidase which are used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lysyl oxidase; lipoxygenase; protein disulfide isomerase; phenol oxidase; peroxidase; protein disulfide reductase; tyrosine oxidase; food; sulfhydryl oxidase; animal feed.
                                                                                                                           Manufacture of active preparations comprises cross linking a protein, which surrounds the active substance with an enzyme, especially a novel lysyl oxidase from Pichia pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of specified enzymes, especially lysyl oxidase, as protein crosslinking agents for formulating compositions containing active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                         Klingler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klingler J,
                                           Lueddecke E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. pastoris lysyl oxidase fragment #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lueddecke E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY51973 standard; peptide; 17 AA.
                                                                                                                                                                                                                    Claim 17; Page 17; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.6%;
70.0%;
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Best Local Similarity 70.v.
Free 7; Conservative
                                         Friedrich T, Bewert W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bewert W,
                                                                                    WPI; 2000-257743/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia pastoris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BADI ) BASF AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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Gaps

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21; Length 22; 7; Indels

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Seguence

Query Match

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This sequence is encoded by a cDNA of the invention, designated Gene No. 20. This sequence represents a human secreted protein, and is expressed ubiquitously, including T-cells and amygdala. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzhahmer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders or blood disorders
the polypeptides in a suitable culture system. The composition (used to vaccinate a patient against a proteobacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein encoded by Gene No. 20.
                                                                                                                          DB
                                                                                                                                      Pred. No. 94;
1; Mismatches
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                                                                                                                     27.6%; Score 37; 50.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 157; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                AAW73416 standard; Protein; 23 AA.
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97US-0048356.
97US-0050935.
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97US-0044039
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97US-0048101
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                     3 APGTFSNTTSSTDICRPHQI
                                                                                                                                                                                                                                 Query Match . 27.6
Best Local Similarity 50.0
Matches 10; Conservative
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Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-070209/06.
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                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                      AAW73416;
                                                               Sequence
                                                                                                                                                                                                                                                                                                                           AAW73416
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                                                                       This invention describes a novel method where an enzyme (I) selected from lipoxygenases, protein disulfide isomerases, phenol oxidases and peroxidases, lysyl oxidases, protein disulfide reductases, tyrosine oxidases or sulfinydryl oxidases is used to formulate compositions containing active ingredients. (I) is useful for crosslinking protein layers surrounding active ingredients in food, animal feed and pharmaceutical products. The compositions can be formulated without using chemical crosslinking agents. AA$51963-Y51974 represent fragments of the Pichia pastoris lysyl oxidase protein which is used to
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; extracellular domain; virulence determinant; YadA;
                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adhesin; proteobacterial infection prevention; vaccine.
                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 21;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AA.
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                                   Claim 17; Page 16; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                           30.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB51542 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                    17 AA;
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15-FEB-2001

AAB51542;

AAB51542 ID AAB5 RESULT

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19-OCT-2000.

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can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalithes and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an immunogenic peptide derived from hepatitis B surface antigen (HBSAg) which competes with the hepatitis B surface antigen/annexin V interaction or which binds a compound or antibody competing with the hepatitis B surface antigen/annexin V interaction. Also claimed are: (1) a combination of the immunogenic peptide and a negatively charged phospholipid; (2) a peptide composition comprising the immunogenic peptide; (3) a vaccine comprising the immunogenic peptide (4) antibodies which specifically bind to the peptide and inhibit binding of HBSAg to annexin V, and (5) a therapeutic composition comprising as an active substance the antibodies of (4).

The vaccine of (3), and the therapeutic composition of (5), can be used as an inexculum to vaccinate humans against an infection with hepatitis
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic polypeptide from hepatitis B surface antigen - useful
in, e.g. vaccine against hepatitis B virus or hepatitis delta virus
infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface antigen; immunogen; vaccine;
                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B surface antigen derived peptide (IGP 1082).
                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                    Score 37; DB
Pred. No. 99;
                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis delta virus; infection; HBsAg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; peptide; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97EP-0870103.
96EP-0870164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 43.0
                                                                                                                                                                                                                                                                                                                                       2 CAPGTFSNTTSSTDIC 17
                                                                                                                                                                                                                                                                                                                                                                       5 cgpgaagtacssacic 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annexin V; hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-388040/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis b virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1998
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                                                                                                                                                                                                                 Sequence
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B and/or hepatitis delta virus. The immunogenic peptide can be used in method to detect antibodies which are capable of competing with the hepatitis B and/or hepatitis Delta virus surface antigen/annexin V interaction. The immunogenic peptide can also be used to screen for drugs which block the binding between annexin V and the peptide, and as a therapeutic to treat humans infected with hepatitis B virus and/or hepatitis Delta virus. The present sequence represents one of the peptide fragments derived from HBsAg which were synthesised to map the annexin V-binding site on HBsAg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting Adenomatous Polyposis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that specifically bind to APC protein and detecting the complex formed -
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Joslyn G, Kinzler K, Markham AF, Anand
, Thliveris A, Nakamura Y, Vogelstein B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyposis Coli (APC) protein in a sample. The method involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic predisposition; drug screening; DP2.5; repeat region.
                                                                                                                                                                                                               Length 23;
                                                                                                                                                                                                             Score 34.5; DB 19;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human APC protein 20 aa repeat #4 (1643-1662).
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Column 33-34; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        AAB23019 standard; peptide; 20 AA.
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91GB-0000974.
91GB-0000975.
91US-0741940.
94US-0289548.
                                                                                                                                                                                                             25.7%;
                                                                                                                                                                                                                               44.48;
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UNIV UTAH.
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pllpgt---sttstgpck 15
                                                                                                                                                                                                                                                                              1 PCAPGTFSNTTSSTDICR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 8; Conservative
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White RL,
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                                                                                                                                                                23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2001
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12-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAB23019;
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                                                                                                                                                                  Sequence
                                                                                                                                                                                                               Query Match
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(UTAH
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contacting the sample with antibodies which specifically binds to the 2843 amino acid form of the human APC protein, or to a mutant APC protein, and detecting an APC-antibody complex. Mutations in the APC gene play a role in tumorigenesis, indicating that it is a tumour suppressor gene. It is located on chromosome 5q21, which corresponds to the FAP (familial adenomatous polyposis) locus. FAP is an autosomal dominant inherited disease in which affected individuals develop hundreds to thousands of adenomatous polyps in the colon and rectum, some of which progress to malignancy. The FAP locus is often found to be deleted in sporadic (i.e., non-familial) adenomas and carcinomas, and chromosome 5g deletions have also been observed in tumours of the lung, breast, colon, rectum, bladder, liver, sarcomas, stomach, and prostate, and in leukaemias and lymphomas. Although the FAP locus contains are several other genes such as FER, TB1, TB2, and MCC, it is thought that mutations in the APC gene play a key role in the development of FAP and sporadic tumours. The method is useful for detecting APC protein and its mutations in fortal tissue, placental tissue, amniquic fluid, blood, serum or a timour sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-F; presentlin I; presentlin II; cellular tumour antigen; glial fibrillary acidic protein; GRAP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                      serum or a tumour sample. The method is useful for diagnosing or prognosing neoplastic tissue, for detecting a genetic predisposition to cancer, for detecting germline and somatic alteration of wild-type APC genes, and for testing therapeutic agents for the ability to suppress tumours. Sequences AAB23016-B23022 represent seven 20 amino acid repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frameshift mutation, age-related disease, neurodegenerative disorder, Alzheimer's disease, Down's syndrome, myotonic dystrophy; neuronal, Huntington's disease; multiple sclerosis; alcoholic liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
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Pred. No. 2.7e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    semiregularly spaced in the human APC protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROYAL NETHERLANDS ACAD ARTS & SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY20893 standard; Protein; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.08;
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Best Local Similarity 44.4
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-1997;
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This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, all disease, Down's syndrome, myotonic dystrophy, Huntington's disease, and littles typer II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-mayloid precursor protein (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-t, neurofilament-M, neurofilament-F, presentlin I, presentlin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) protein (CHMSP-C) and neuroendocrine specific protein A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                      Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delgado Boada JM, Campana HR, Curbelo DM, Jimenez ER;
Patron CF, Cremata Alvarez JA, Garcia Fernandez R;
Garcia Garcia BM, Gonzalez Martinez ME, Herrera Martinez LS;
Margollez Clark E, Morera Cordova V, Raices Perez-Castaneda MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.6%; Score 33; DB 19; Length 15; 83.3%; Pred. No. 2.3e+02; 1ve 0; Mismatches 1; Indels
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                                                                                                                                                                                           Disclosure; Figure 10; 258pp; English.
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                WPI; 1998-609901/51.
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                                      N-PSDB; AAX75761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CAPGTF 7
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Migration stimulatory factor; MSF; cell migration; modulation; human; wound healing; scarring; MSF1-alpha; epitope; fibronectin.
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                                                                                          AAY28912 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    wound and preventing scarring
                                                                                                                                                                                                                                                                                                                             97GB-0026539
                                                                                                                                                              MSF 1-alpha peptide epitope
                                                                                                                                       21-SEP-1999 (first entry)
                        | || :||:|| |
plipg---stttstgpc 23
            1 PCAPGTFSNTTSSTDIC 17
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                           Schor SL;
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-430039/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be raised
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                      15-DEC-1998;
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                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           Schor AM,
                                                                                                                 AAY28912;
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                                 10
                                                                     RESULT 1
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                                                                 The N-terminal region of P. minioluteum dextranase was sequenced using the Edman degradation method. Dextranase may be secreted as a recombinant protein by the transformed host, Pichia pastoris. The recombinant enzyme has higher thermal stability than the natural P. minioluteum enzyme (specifically an optimum temp. of 55-60 deg and a half-life of 7.6 hr at 50 deg), and it can be used in the sugar industry for sugarcane juice dextran hydrolysis.
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic peptide carrying an epitope of hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim peptides comprising not more than 30 AA units and contg. a sequence in AAP50658-50662. Also claimed are watersoluble oligomers of the peptides, comprising 2-10 monomer units, and prods. comprising the peptides covalently coupled to a biologically acceptable carrier, pref. with mol. wt. greater than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fmmunogenic peptide(s) - carrying epitope of hepatitis B surface
          Nucleotide sequence encoding Penicillin minioluteum dextranase useful for the high-level industrial prodn. of dextranase.
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                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.5; DB 6;
Pred. No. 4.2e+02;
2; Mismatches 4;
                                                                                                                                                                                               Score 33; DB 16;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chedid
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B vaccine; antigen; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Audibert F,
                                                                                                                                                                                                                                                                                                                            AAP50661 standard; peptide; 23 AA.
                                            Example 2; Page 7; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ANVR ) AGENCE NAT VALORISATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 24; 26pp; French.
                                                                                                                                                                                                24.6%;
46.2%;
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Similarity 47.1%;
8t, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83FR-0012659
                                                                                                                                                                                   Ouery Match
Best Local Similarity 40...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gras-Masse H,
                                                                                                                                                                                                                                                                                                                                                                                                             virus surface antigen.
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2 gttnnthcgadfc 14
                                                                                                                                                                                                                                             5 GTFSNTTSSTDIC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1985-070199/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8t Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                               Ψ
                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2550203-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tartar A,
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                 AAP50661;
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                                      The invention provides a human migration stimulatory factor (MSF) protein. Host cells containing a replicable vector comprising the MSF encoding nucleic acid can be used for the recombinant production of the protein. The polypeptide can be used for modulating cell migration, healing a wound and for preventing scarring. Sequences AAY28912-913 represent peptide epitopes of MSF against which monoclonal antibodies
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                         Score 32.5; DB 20
Pred. No. 4.2e+02;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW07656 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ATM gene product epitope 1.
Claim 29; Page 61; 86pp; English.
                                                                                                                                                                                                                                                                           24.38;
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                                                                                                                                                                                                                                                                                                                          Conservative
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08-APR-1996;
                                                                                                                                                                    16-MAY-1995;
                                                                                                         21-NOV-1996.
                                                                                                                                                                                                                              Shiloh Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW77164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and monoclonal antibodies. Antibodies raised against the ATM protein detected mono-specifically a high molecular weight of the expected size of 350 kDa on Western blots of protein lysates derived from fibroblast and lympho- blastcid cell lines. Because derived from fibroblast truncation mutations in the ATM gene, mutated ATM protein can be identified if such proteins are stable. Mutations in the ATM gene cause ataxia- telangiectasia (A-T), a progressive genetic disorder affecting the central nervous and immune systems. The ATM gene, located at chromosome ilga22.33, is probably involved in a novel signal transduction system that links DNA damage surveince to cell cycle control. The ATM gene product (AAW07655) has a highly conserved C-terminal region showing hinases. A-T mutations affect a variety of tissues and lead to cancer predisposition. Identification of A-T carriers, by analysis at nucleic acid or protein levels, allows better supervision and treatment of such subjects who are at increased risk of developing cancer and are particularly sensitive to radiation. The transgence animals and transformed cells are useful as models of the human disease. Also viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATM gene; ataxia-telangiectasia; progressive genetic disorder; antibody; central nervous system; immune system; chromosomal instability; therapy;
                                                                                                                                                                                                                                                                                                                                      AAW07656-62 are human ATM protein epitopes used to generate polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vectors expressing the ATM protein can be used in gene therapy of A-T.
                                                                                                                                                                                                                                                               New gene ATM implicated in ataxia-telangiectasia and related protein - useful in screening methods, partic. for identifying disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
phosphatidylinositol-3 kinase; PI-3; cancer predisposition; carrier;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 18;
Pred. No. 3.2e+02;
                                                                                                                                                                               (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
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                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                             Claim 24; Page 86; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW06235 standard; peptide; 15 AA.
                                                                                                                                                                                                                  Tagle DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%;
                                                                                                         96WO-US07040
                                                                                                                                           95US-0441822.
                                                                                                                                95US-0508836
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            untranslated region; UTR.
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                                                                                                                                                                                                                Shiloh Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'... 5; Conserve
                                                                                                                                                                                                                                        WPI; 1997-012074/01.
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6 ssasqstdlc 15
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                                  Homo sapiens
                                                          WO9636695-A1
                                                                                                                                                                                                               Collins FS,
                                                                                                         16-MAY-1996;
                                                                                                                                           16-MAY-1995;
21-JUN-1995;
                                                                                                                                28-JUL-1995;
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                                                                                 21-NOV-1996
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                                                                                                                                                                                                                                                                                         carriers
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DE ATM
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KW ATM
KW ATM
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targetted against ATM. Ataxia-telangiectasia (A-T) is caused by antibodies targetted against ATM. Ataxia-telangiectasia (A-T) is caused by antibodies targetted against ATM. Ataxia-telangiectasia (A-T) is caused by cataxia-telangiectasia (A-T) is caused by the ATM of the ATM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
cancer predisposition; radiation sensitivity; cell cycle abnormality; until-system disease; autosomal recessive; cerebellar ataxia; cerebellum; general motor dysfunction; Purkinje cell; oculocutaneous telanglectasia; blood vessel; bulbar conjunctiva; facial skin; A-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pharmacuetically active peptide; target; organ; lymphocyte; treatment; pharmaceutical agent; disease; radioactive isotope; imaging agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated ataxia-telangiectasia gene - used to develop prods. for the study, diagnosis and treatment of ataxia-telanglectasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW06235-W06238 represent epitopes of the ATM protein (see AAW06234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KOHN/) KOHN K I.
(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 16; 153pp; English.
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50.0%;
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95US-0441822
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Best Local Similarity
Local 5; Conserve
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Search completed: July 13, 2001, 17:16:50 Job time: 140 sec
10-SEP-1998;
                                             Vogel T,
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                                                                                                                                                                                                                                                                                                            non-naturally occurring pharmacuetically active peptides. These novel peptides specifically bind to undetermined and determined targets in various organs and in lymphocytes. The peptides can be used in compositions, where they can be linked to pharmaceutical agents, to treat various diseases and conditions. The peptides or chimeric polypeptides or comprising these pharmaceutically active peptides and a second peptide may be labelled with a marker (radioactive isotope, etc) to form an imaging agent. This agent is used to bind an organ so that the organ can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue specific epitope; umbilical cord; human; endothelial cell; vein; tumor cell; tumor tissue; delivery agent; imaging; artery; radial; liver; coronary; mammary; safenal; femoral; placenta; kidney; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               New peptide(s) binding targets in organs and lymphocytes - for the targetted delivery of toxins, anti-cancer drugs and cardiovascular agents to arteries, veins, placenta, liver
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                                                                                                                                                                                                                                                                                                     Sequences shown in AAW77160 to AAW77214 and AAW79167 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human umbilical cord specific epitope from clone TUV-R4B*-#23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                         , Lazarovits J, Levanon A;
Zeelon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 19; Length 15
Pred. No. 3.2e+02;
2; Mismatches 5; Indels
                                                                                                                                                  (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                            Claim 10; Page 92; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY33126 standard; Protein; 15 AA.
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                                                                                                                                                                         Hagai Y,
                                                                                                                                                                      Belkind A, Golan I, Hagai Y
Nimrod A, Panet A, Vogel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.9%;
                                                                                         98WO-US04188
                                                                                                                97US-0810074
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Best Local Similarity 50.0
Matches 7; Conservative
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2 sttrnrtdinkptg 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              central nervous system
                                                                                                                                                                                                         WPI; 1998-495863/42
                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
                        Homo sapiens
                                            WO9839469-A1
                                                                                                               04-MAR-1997;
                                                                                                                           04-MAR-1997;
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                                                                                         04-MAR-1998;
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          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                           be imaged
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This invention describes novel non-naturally occurring pharmaceutically active peptide epitopes (1) comprising the tripeptide, Glu-Gly-Arg. (1) are useful for binding to endothelial call and tumor cells/fissues, and are also useful for imaging an organ, preferably an artery (umbilical cord artery, radial artery, coronary artery or mammary artery), a vein (umbilical cord vein, safenal vein or femoral vein), placenta, tumor tissue, kidney, heart or liver. The artery is preferably damaged, and is a coronary artery rhey are also useful for treating an organ in vivo, preferably an artery (umbilical cord artery, radial artery, coronary artery or an enamary artery, preferably a damaged coronary artery (umbilical cord artery, radial artery, coronary artery, inclinated ord artery or a mammary artery, preferably a damaged coronary artery, wein tissue, kidney, heart, liver, or central nervous system. AAY33123-Y33132 represent epitopes described in the method of the invention.
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                                                                                                                                                                                                                                                                                                       peptides useful for directing therapeutics to cancer tissues - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 3.2e+02;
2; Mismatches 5; Indels
                                                                          (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 67; 70pp; English.
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50.0%;
98US-0154404
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                                                                                                                                                                                                                            WPI; 1999-540813/45
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                          endothelial cells
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STATE: Pennsylvania
COUNTRY: USA
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Sequence 3, Appli
Sequence 4, Appli
                                                                                   July 13, 2001, 17:14:50; Search time 12.12 Seconds (without alignments) 38.228 Million cell updates/sec
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Sequence 178, App
Sequence 178, App
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Patent No. 5217891
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Sequence 83, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 4
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US95-04018-45
US-08-221-583-44
PCT-US95-04018-44
PCT-US95-04018-44
PCT-US95-04018-44
PCT-US95-04018-44
US-08-221-583-47
PCT-US95-04018-48
PCT-US95-04018-48
US-09-101-146-58
US-08-31-33
US-08-31-34
US-08-393-44
US-08-393-44
US-08-508-835A-4
US-08-508-835A-4
US-08-508-835A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-629-001A-4
US-08-635-178
US-08-444-631-178
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US-08-612-973-83
US-08-323-531-8
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134
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                      length: 0
length: 23
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Maximum DB seq
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No.
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Sequence 8, Appl1
Sequence 8, Appl1
Sequence 8, Appl1
Sequence 244, App
Sequence 244, App
Sequence 7, Appl1
Sequence 10, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 280, Appl
Sequence 315, Appl
Sequence 31, Appl
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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ZIP: 19403
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25:mdctcMod.
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 1; Length 15;
Pred. No. 0.00075;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heaver, George A.
TILE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
  US-08-198-094-8
US-08-107-794A-8
PCT-US93-07424-8
US-08-484-635-244
US-08-844-631-244
US-08-874-763-7
US-08-74-763-7
US-08-74-763-7
US-08-75-0244
US-08-74-763-7
US-08-75-0244
US-08-602-999A-280
US-08-602-999A-315
PCT-US95-04018-49
US-08-602-999A-315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3400
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.7%;
93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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MOLECULE TYPE: peptide

US-08-221-583-45
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TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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Best Local Similarity 93.3
Matches 14; Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsvlvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
Sequence 46, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Necrosis Factor Inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTATION UNDRER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TENETHONE: (215) 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72;
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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Meber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERfect 5.1
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Best Local Similarity 93.3
Matches 14; Conservative
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APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-46
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                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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PCT-US95-04018-45
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72; DB 5; I
Pred. No. 0.00075;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania
PAPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, MATK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CCOR-0232 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Heavner, George A. APPLICANT: Kruszynski, Marian APPLICANT: Mervic, Miljenko APPLICANT: Weber, Robert W. TITLE OF INVENTION: Tumor Necroi NUMBER OF SEQUENCES: 76
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-221-583-47
                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Heavner, George A.

TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                    Score 72; DB 5; Length 15; Pred. No. 0.00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 71; DB 1; Length 15; 100.0%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                          0; Mismatches
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CLASSIFICATION: 514
ATTORNEY, APGENT INFORMATION:
NAME: DeLUCE, MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
             REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/08221583 Patent No. 5486595 GENERAL INFORMATION:
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                      53.78;
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                          MOLECULE TYPE: peptide PCT-US95-04018-46
                                                                                                                                                                                                                                                                                                                              8 SNTTSSTDICRPHOI 22
                                                                                                                                                                                                                                                                                                                                                                1 SNTTSSTDIARPHQI 15
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: USA
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                                                                                                                                              amino acid
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Matches 14; Conserv
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US-08-221-583-44
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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Pred. No. 0.001;
0; Mismatches 0; Indels
                                                                                                                                        Tumor Necrosis Factor Inhibitors
                                                                                                                                                                NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: Norris
                                                                                                                                                                                                                                                 STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
Sequence 44, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/08221583
Patent No. 5486595
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100.08; Fi.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.0%;
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Best Local Similarity 100.
Matches 14; Conservative
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Gaps

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APPLICANT: WALLACH, DAVID
APPLICANT: NOPHAR, YARON
APPLICANT: KEMEER, OLIVER
APPLICANT: ENGELMANN, HARMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADBRKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF ENVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and No.
                                                                                                                                                                                                                                                                                                                                                                    Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMEDUTE: IBM PC Compatible
COMEDUTE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB Seried. No. 0.07
                     NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
RELECOMMUNICATION INFORMATION:
TELEPRIONE: (215) 568-3409
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-126-016-24; Sequence 24, Application US/08126016; Patent No. 5811261
                                                                                                                                                                                                                                                                                                                                                                  42.5%;
ilarity 91.7%;
Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TSSTDICRPHQI 22
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                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
Matches 11; Conserv
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PCT-US95-04018-47
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MOLECULE TYPE:
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                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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PCT-US95-04018-47
Sequence 47, Application PC/TUS9504018
Sequence 47, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.5%; Score 57; DB 91.7%; Pred. No. 0.07:1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FIQURA DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids
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Best Local Similarity 91.7
Matches 11; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                        ZIP: 19403
COMPUTER READABLE FORM:
  Pennsylvania
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| TSSTDIARPHQI 12
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                                                                                            MEDIUM TYPE:
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                     COUNTRY:
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Marlton
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                                                                             COUNTRY:
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                               APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.8%; Score 44; DB 1; Length 15; 88.9%; Pred. No. 3.9;
                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Wervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
                                                        ore 48; DB 2;
red. No. 1.6;
Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             Sequence 48, Application US/08221583 Patent No. 5486595
                                                         35.e.,
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                    Query Match 35.8
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-48
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 TDICRPHQI 22
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| TDIARPHQI 9
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PCT-US95-04018-48
US-08-126-016-24
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Gaps
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Sequence 58, Application US/09101146
Sequence 58, Application US/09101146
Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCESS:
ADDRESSEE: Jane Massey Licata, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/10/10/146
FILING DATE: October 7, 1998
One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.8%; Score 44;
88.9%; Pred. No.
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Jane Massey Licata,
66 E. Main Street
                                                                                   ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 15 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTI
COMPUTER: IBM PC
                                              Pennsylvania
USA
      : One Libert
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Gaps

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Score 33; DB 1; Length 10, Pred, No. 1.2e+02;
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1.5e+02;
5;
                                                                                                                                                                                                                                                                       GENERAL IRPORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STAFF: FACTORY
                                                                                                                                                                                                                                                                                                                                                                                     SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2;
                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                     Sequence 141, Application US/08934915
Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/08493092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFRENCE/DOCKET NUMBER: 1346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                  Query Match
Best Local Similarity 46.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 53.8.
Tr Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                   5 GTFSNTTSSTDIC 17
                                                                                                                                                            8 SNTTSSTDICRPH 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SNEVSSPEIIRQH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLORIDA
                                                                                                                                                                                                                                     RESULT 14
US-08-934-915-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-934-915-141
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US-08-493-092-4
US-08-354-618-3
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                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 4; Length 23; Pred. No. 29; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Clark, Emilio Margollez
APPLICANT: Curbelo, Dania Mateu
APPLICANT: Boada, Julio Marcos Delgado
APPLICANT: Martinez, Luis S. Herrera
APPLICANT: Alvarez, Jos Alberto Gremata
APPLICANT: Perez-Casta eda, Manuel Rafael Raices
APPLICANT: Martinez, Maria Elena Gonz lez
APPLICANT: Jim nez, Efrain Rodriguez
TITLE OF INVENTION: Dextranase enzyme, method for it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: diskette' - 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campana, Hernan Roca
Garcia, Bianca Maria Garcia
Clark, Emilio Margollez
Curbelo, Dania Mateu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect 6.0 version B CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/354,618
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELEPAX: (866) 810-11515
TELEFAX: (866) 810-11515
TELEFAX: (866) 810-11515
TELEFAX: (866) 810-11515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08354618
; Patent No. 5637491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 115/93
FILING DATE: 14-December-1993
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Ronald J. Baron
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
                                                                                                                                                                                                                                                                                                                                                                       29.18;
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.8°
"Thes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CAPGIFSNITSSIDIC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CAAGITIGATGTTATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                         Amino Acid
                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11753
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Gaps

Search completed: July 13, 2001, 17:17:09 Job time: 139 sec

8 SNTTSSTDIC 17 |::||:| 6 SSASQSTDLC 15

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

July 13, 2001, 17:12:20 ; Search time 13.32 Seconds (without alignments) 223.034 Million cell updates/sec Run on:

US-09-800-909-2\_COPY\_163\_201 216 1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters

8589

Minimum DB seq length: 0 Maximum DB seq length: 39

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cell surface	0	hypothetical prote	യ	ical	agelenin - funnel-	מי	Ca2+/calmodulin-de	napin large chain	t-complex polypept	somatotropin intro	pheromone precurso	r-cell receptor be	antifungal protein	conceptus protein	ப	beta-defensin-1 -	T-cell antigen rec	30K allergen - rye	glucagon-like pept		OWIN	lectin - sunn hemp	Ca2+/calmodulin-de	gene X protein - h	S	hypothetical prote	alpha-conotoxin EI	homeodomain protei
SUMMARIES	QI	G49050	A37479	568261	A05323	G82613	A60959	A22977	A42865	S70343	E49410	A60716	A48158	B49048	S28994	C61233	A39830	A45495	S47381	S38292	A60317	I54351	A39269	S08293	B42865	323	341	D81044	58	056
	BB	7	7	~	7	7	~	~	~	~	~	~	~	ĆΙ	~	7	~	~	~	~	~	~	N	7	7	N	~	~	Н	7
	Match Length	37	33	37	39	39	35	30	20	30	34	39	38	18	56	29	35	38	13	16	17	21	22	24	26	31	32	34	18	23
* Ouerv	Match		17.6	15.7		•	15.0	14.8	14.4	14.4	14.4	14.4	4.	ص	13.9	٠		13.9	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.0	13.0
	Score	38.5	38	34	33.5	33	32.5	32	31	31	31	m	30.5	30	30	30	30	30	29	29	29	29	29	29	29	29	29	29	28	28
Result	No.	٠.	7	Э	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

25 2 S74094 27 2 S28995 27 2 C44636 27 2 T12330 29 1 GCFLE 30 1 TIPUIM 30 2 A47607 31 2 S28991 31 2 A55430 32 2 A82208 36 2 A7614 36 2 A82208 36 2 A82208	fibulin 1 variant antifungal protein homeotic protein H metallothionein - glucagon - Europea glucagon - Europea trypsin inhibitor immunogenic protei trypsin inhibitor hypothetical protei	conotoxin NgVIA alpha-lactalbumin hypothetical prote Ig heavy chain V-I notechis II-55 non
попрининания	S74094 S28995 C44636 C12330 GCFLE A61135 A7607 S21743 S2899	A55430 PL0164 A82208 JT0513 A39328
	аппананана	00000
	700000000000000000000000000000000000000	12.7 12.7 12.7 12.5
2.7.7.7.0000000000000000000000000000000	20 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	27.5 27.5 27.5 27.5 27.5
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4444 04444 04354

## ALIGNMENTS

```
T-cell surface glycoprotein CD8 beta-1 chain, secreted form 5 - human (fragment)
```

C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence\_revision 03-Nov-1995 #text\_change 29-Aug-1997
C;Accession: 649050
Eur. J Immunol. 23, 320-326, 1993
A;Title: Transcriptional diversity at the duplicated human CD8 beta loci.
A;Reference number: A49050; MUID:93170376
A;Reference number: A49050; MUID:93170376
A;Reference number: A49050; MUID:93170376
A;Reference number: A49050; MUID:93170376
A;Reference number: A5050; MUID:93170376
A;Re

A; Note: sequence extracted from NCBI backbone (NCBIP:125543)
C;Genetics:
A;Gene: GDB: CDBB1; CDBB
A;Cross-references: GDB:119771; OMIM:186730
A;Map position: 2p12-2p12
C;Keywords: alternative splicing; extracellular protein; glycoprotein

Gaps 'n Length 37; Query Match 17.8%; Score 38.5; DB 2; Length 3 Best Local Similarity 34.8%; Pred. No. 2.1e+02; Matches 8; Conservative 5; Mismatches 7; Indels

1;

1 PCAPGTFSNTTSSTDICRPHQIC 23 δ

13 PLSPNACMDTTA---ILQPHRSC 32 QQ

RESULT 2
A3749
huwentoxin-I - Chinese bird spider
C;Species: Selenocosmia huwena (Chinese bird spider)
C;Species: Selenocosmia huwena (Chinese bird spider)
C;Date: 18-Mar-1994 #sequence\_revision 07-oct-1994 #text\_change 16-Feb-1996
C;Accession: A37479; JC1089
R;Liang, S.P.; Zhang, D.Y.; Pan, X.; Chen, Q.; Zhou, P.A.
Toxicon 31, 969-978, 1993
A;Title: Properties and amino acid sequence of huwentoxin-I, a neurotoxin purified fr
A;Reference number: A37479; MUID:94024948
A;Accession: A37479; MUID:94024948
A;Accession: A37479
A;Residues: 1-33 <LIA>
A;Residues: 1-33 <LIA>
A;Luo, J.C.; Jing, H.; Gu, X.C.
Acta Soi, Natur. Univ. Pekin. 29, 668-674, 1993
A;Title: Secondary structure study of huwentoxin-I, a neurotoxin from the venom of th

A;Accession: JC1089 A;Moleous: type: protein A;Residues: 1-33 <LI2> C;Comment: This peptide is the major active protein component of venom in this specie

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A. Experimental Source: Strain 955

R. Simpson, A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.S.; Bueno, M.F.P.; Camargo, A.A.; Camargo, L.E.A.; Carararo, D.M.; Carrer sa-Netc, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

J. J. Strain A.D.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieqer, J.E.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

R. Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mnenck, C.F.M.; Miracca, E.C.; Martins

Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A; Ruthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Salva Jr., W.A.; da Silva, A.L., 
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Réference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A60959
R;Haglwara, K.; Sakai, T.; Miwa, A.; Kawai, N.; Nakajima, T.
Biomed. Res. 11, 181-186, 1990
A;Title: Complete amino acid sequence of a new type of neurotoxin from the venom of t A;Reference number: A60959
A;Accession: A60959
                                                                                                                                                                                                           A;Status: preliminary
A;MoLecule type: DNA
A;Residues: 1.39 <SINA
A;Cross-references: GB:AE004018; GB:AE003849; NID:99107093; PIDN:AAF84790.1; GSPDB:GN
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agelenin - funnel-weaving spider (Agelena opulenta)
C;Species: Agelena opulenta
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 24-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Residues: 1-35 <HAG>
C;Keywords: calcium channel inhibitor; presynaptic neurotoxin; venom
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Pred, No. 1.1e+03;
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Pred. No. 1.2e+03;
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A; Reference number: A22977; MUID:85104736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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37.5%;
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42.9%;
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Best Local Similarity
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S68261

Whypothetical protein gadd7.2 - long-tailed hamster
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68261
R;Hollander, M.C.; Alamo, I.; Fornace Jr., A.J.
Nucleic Acids Res. 24, 1589-1593, 1996
A;Title: A novel DNA damage-inducible transcript, gadd7, inhibits cell growth, but lacks A;Reference number: S68260; MuID:96211359
A;Accession: S68261
A;Accession: S68261
A;Accession: Dreliminary
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A; Residues: 1-39 <SOS>
C; Comment: Phospholipases A2 catalyze the calcium-dependent hydrolysis of the 2-acyl grc
C; Superfamily: phospholipase A2
C; Keywords: calcium; carboxylic ester hydrolase; lipid degradation; venom
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phospholipase A2 (EC 3.1.1.4) - Mexican beaded lizard (fragment)
N.Alternate names: phosphatidylcholine 2-acylhydrolase
N.Alternate names: phosphatidylcholine 2-acylhydrolase
C.Specises: Heloderma horridum (Mexican beaded lizard)
C.Specises: Heloderma horridum (Mexican beaded lizard)
C.Saccession: A05333
S. Accession: A05333
Blochemistry 25, 2927-2933, 1986
A.Reference number: A05323; MUID:86243292
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G82613
hypothetical protein XF1988 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Auy-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: (202613
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                                                                                                                                    Score 38; DB 2; Length 33;
Pred. No. 2.2e+02;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
          C; Keywords: presynaptic neurotoxin; venom F; 2-17, 9-22, 16-29/Disulfide bonds: #status experimental
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Pred. No. 7.9e+02;
0; Mismatches 4;
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                                                                                                                                       17.6%;
30.0%;
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60.0%;
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                                                                                                  Query Match
Best Local Similarity 30.00,
The 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-37 <HOL>
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t-complex polypeptide 1 homolog (peak 2 fraction) - rabbit (fragments)
N;Alternate names: chaperonin homolog (peak 2)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
C;Accession: E49410
C
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A,Accession: A48158
A,Status: preliminary
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C; Comment: The mRNA encoding this hypothetical protein shows homology at the nucleoti
he complete mRNA may encode a protein related to somatotropin through abnormal splici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             somatotropin intron-related protein RDE.25 - rat (fragment)
N;Alternate names: growth hormone gene-related protein RDE.25
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14 May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: A60716
R;Montpetit, M.L.; Tenniswood, M.P.
J. Cell. Biochem. 39, 285-292, 1989
A;Title: Does the lack of regression-associated mRNA expression render a rat ventral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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C;Species: Filobasidiella neoformans, Cryptococcus neoformans
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A;Residues: 1-34 <ROM>
A;Residues: 1-34 <ROM>
A;Experimental source: reticulocyte
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIP:141043)
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A;Accession: A60716
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Mol. Cell. Biol. 13, 1962-1970, 1993
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Matches 7; Conserve
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A; Status: preliminary
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C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Oate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-Dec-2000
C;Accession: S70343; S70343
R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 34-43, 1996
A;Title: Purification and sequencing of multiple forms of Brassica napus seed napin larg
A;Reference number: S70340; MUID:96283791
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase (autophosphorylation sites) - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A42865
Ca2+/calmodulin-dependent myosin light chain kinase (autophosphorylation sites)
C;Specias: Orycolagus cuniculus (domestic rabbit)
C;Specias: Orycolagus cuniculus (domestic rabbit)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: A42865
R;Gao, Z.H.; Moomaw, C.R.; Hau, J.; Slaughter, C.A.; Stull, J.T.
B;Ochemistry 31, 6126-6133, 1992
A;Title: Autophosphorylation of skeletal muscle myosin light chain kinase.
A;Reference number: A42865; MUD:92329432
A;Reference number: A42865
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 GAQA>
A;Experimental source: skeletal muscle
A;Mote: sequence extracted from NCBI backbone (NCBIP:109204)
C;Keywords: calmodulin binding
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Pred. No. 1.6e+03;
3; Mismatches 3; Indels
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A;Molecule_ftype: protein
A;Residues: 1-30 <ARM>
C;Superfamlly: 20K parasporal crystal protein
C;Keywords: delta-endotoxin
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A;Residues: 4-19 <NE2>
C;Superfamily: wheat alpha-amylase inhibitor
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A; Residues: 1-19;20-24;25-30 <NEU>
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A; Status: preliminary
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C; Species: Homo saplems (man)
C; Species: Homo saplems (man)
C; Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C; Accession: B49048
R; Sidud, M.; K; Bidsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A; Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A; Reference number: A49048; MUID:92387250
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C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: $28994
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae A;Reference number: $28989; MUID:93138130
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: C61233
R;Thatcher, Maj.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; Randal,
A; Note: sequence extracted from NCBI backbone (NCBIN:126064, NCBIP:126070)
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                                                                           Length 38;
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A;Residues: 1-18 <SIO>
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Pred. No. 1.3e+03;
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                                                                        Score 30.5; DB 2;
Pred. No. 2.2e+03;
4; Mismatches 9;
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A,Residues: 1-26 CTER>
C,Superfamily: gamma-thionin
C,Keywords: phosphoprotein
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Z Z Z	[2]	Protein Chem.	ווו ס מנו	nem.	77:71	17-05		1993).					
RX R	MEDI Zho	AACTE LINE	RIZA 9717 A.,	CHARACTERIZATION. MEDLINE=97179771; Zhou PA., Xie X	PubMed-9028007	fed={ Li	902i M.	8007; , Yang D	Σ	, Xie ZF	x guoz	.:	
K K K	"Blc	ng s. ockad veno	e of	neur the	Chine	ulai se k	r ti	ransmiss 1 spider	ion	Liang S. P.; "Blockade of neuromuscular transmission by huwentoxin-1, the venom of the Chinese bird spider Selenocosmia huwena		rit	purified from
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Discovery and characterization of a family of insecticidal neurotoxins with a rear vicinal disulfide bridge.";
Nat. Struct. Biol. 7:505-513(2000).
-!- FUNCTION: INSECTICIDAL NEUROTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
NCBI_TaxID=6904;
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01-0CT-2000 (Rel. 40, Last annotation update)
1-ATRACOTOXIN-HVLC (J-ACTX-HVLC)
Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
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                                                                                                                                                                                    Venom; Neurotoxin; Postsynaptic neurotoxin; 3D-structure.
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Pred. No. 84;
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MEDLINE=20343014; Pubmed=10881200;
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                                                                                                                         Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H., Nicholson G.M., Christie M.J., King G.F.; "Discovery and characterization of a family of insecticidal neurotoxins with a rare vicinal disulfide bridge."; Nat. Struct. Blol. 7:505-513(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
NCBL_TaxID=6904;
                                            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Hadronyche.
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
1-ATRACOTOXIN-WIB (J-ACTX-HVIB)
Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
J-ATRACOTOXIN-HVIA (J-ACTX-HVIA).
Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
                                                                                                                                                                                                                                                                                                                                                                                      Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
DIS98B2560BFE997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
D23442560B89997 CRC64;
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; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA.
                                                                                                                                                                                                                                                                                                                                                                                        DB
96;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom gland;
MEDLINE=20343014; PubMed=10881200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.7%;
nilarity 83.3%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                        17.1%;
40.0%;
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14
33
3685 MW;
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22
14
33
3651 MW;
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                                                                                                                                                                                                                                                              Toxin; Neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
15 Conserve
8; Conserve
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Best Local Similarity
5, Conserve
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14.48;
                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                        3 CLPHNRFCNALSGP 16
                                                                                                                                                                                                                                                                                                 17 CRPH-QICNVVAIP
                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                    35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IX + H(2)O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                               TISSUE-Venom
                                                                                                                                                                                                                                                                                                                                                                             PPOX_BOVIN
P56602;
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SEOUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                           Matches
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2
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-i- CATALYTIC ACTIVITY: PHOSPHAIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-PHOSPHOCHOLINE + A FATTY ACID ANION.
-i- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PIR: A05323; A05323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                     Sosa B.P., Alagon A.C., Martin B.M., Possani L.D.; Blochemical characterization of the phospholipase A2 purified from the venom of the Mexican beaded lizard (Heloderma horridum horridum
                                        20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHOLIPASE A2 (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Venom;
Hagiwara K., Sakai T., Miwa A., Kawai N., Nakajima T.;
Hagiwara K., Sakai T., Miwa A., Kawai N., Nakajima T.;
"Complete amino acid sequence of a new type of neurotoxin from the Complete spider, Agelena opulenta.";
Biomed. Res. 11:181-186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Venom;
Hagiwara K., Inui T., Nakajima K., Kimura T., Kitada C., Fujino M.,
Sakakibara S., Nakajima T.;
"Agelenin, a spider neurotoxin: determination of the C-terminus as
                                                                                                 Heloderma horridum horridum (Mexican beaded lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Agelenidae; Agelena.
NCBL_TaxID=29934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.5; DB 1; Length 39;
Pred. No. 3e+02;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 8F9BC66B5DFB603E CRC64;
                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00119; PA2_ASP; PARTIAL.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Venom.
ACT_SITE 36 36 BY SIMILARITY.
SEQUENCE 39 AA; 4179 MW; 8F9BC66B5DFB603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
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                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CGAGNAASDYSQLGTEKDTDMCCRDHDHC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPGTFSN-----TTSSTDI-CRPHQIC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                      PRT;
                                                                                                                                                                                           MEDLINE-86243292; PubMed-3087412;
                                                                                                                                                                                                                                                   Biochemistry 25:2927-2933(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS, AND AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agelena opulenta (Spider)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 31.0
Matches 9; Conservative
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                HSSP; P00630; 1POC.
InterPro; IPR001211;
                                                                                                                                              NCBI_TaxID=8552;
                                                                                                                                                                                TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TXAG_AGEOP
P31328;
                     PA2_HELHO
P04362;
                                                                                          (FRAGMENT)
                                                                                                                                      Heloderma
                                                                                                                                                                                                                                        Wiegmann)
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                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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TXAG_AGEOP
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          PA2_HELHO
RESULT
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Taketani S., Yoshinaga T., Furukawa T., Kohno H., Tokunaga R., Nishimura K., Inokuchi H.; "Induction of terminal enzymes for heme blosynthesis during differentiation of mouse erythroleukemia cells."; Eur. J. Blochem. 230:760-765(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IX TO FORM PROTOPORPHYRIN IX.
-!- CATALYTIC ACTIVITY: PROTOPORPHYRINGEN-IX + O(2) - PROTOPORPHYRIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- COFACTOR: CONTAINS ONE FAD PER HOMODIMER (BY SIMILARITY).
-:- PATHWAY: PENULTIMATE STEP IN HEME AND PORPHYRIN BIOSYNTHESIS.
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: BOUND TO THE MITOCHONDRIAL INNER MEMBRANE WITH ITS ACTIVE SITE FALING THE CYTOSOLIC SIDE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE PROTOPORPHYRINGEN OXIDASE FAMILY.
POTPHYTIN biosynthesis; Heme biosynthesis; Oxidoreductase;
amide form, and investigation of the disulfide bond arrangement."; Biomed. Res. 12:357-363(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROTOPORPHYRINGEN OXIDASE (EC 1.3.3.4) (PPO) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                          Venom; Neurotoxin; Calcium channel inhibitor; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION.
CBE6462825350D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.5; DB 1;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEDFC3F09CB6A345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                DISULFIDE BONDS, AND AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                             MEDLINE-93043890; PubMed-1421801;
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MEDLINE=95331315; PubMed=7607249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 37, Created)
(Rel. 37, Last sequ
(Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                      24
34
35
3825 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%;
42.9%;
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Tam J.P., Lu Y.-A., Yang J.-L., Chiu K.-W.;

"An unusual structural motif of antimicrobial peptides containing end-to-end macrocycle and cystine-knot disulfides.";

Proc. Natl. Acad. Sci. U.S.A. 96:8913-8918(1999).

-!- FUNCTION: PROBABLY PARTICIPATES IN A PLANT DEFENSE MECHANISM. HAS ANTIBIOTIC ACTIVITY. INHIBITS NEUROTENSIN BINDING. ACTIVE AGAINST BOTH GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.

-!- FUNK: THIS IS A CYCLIC PEPTIDE.

-!- SIMILARITY: BELONGS TO THE CYCLOTIDE FAMILY.

-!- CAUTION: THIS PEPTIDE BEING CYCLIC, ITS SEQUENCE WAS ARBITRARILY CHOSEN TO START AT THE POSITION SHOWN BELOW. AS THE DNA SEQUENCE FROM WHICH IT IS DERIVED IS NOT YET KNOWN, IT IS NOT POSSIBLE TO ASSIGN THE CORRECT N- AND C-TERMINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification, primary structures, and antibacterial activities of beta-defensins, a new family of antimicrobial peptides from bovine neutrophils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J., Smith W., Henschen A.H., Cullor J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 268:6641-6648(1993).
-!- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST
-!- BUT NOT AGAINST S.AUREUS 502A.
-!- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. .
                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

ACCOBBB232ED0CD0 CRC64;
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BY SIMILARITY.

BY SIMILARITY.

48B872D1025E1A68 CRC64;
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Pred. No. 8.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
BETA-DEFENSIN 1 (BNDB-1) (BNBD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HEREFORD; TISSUE-Neutrophils; MEDLINE-93203264; PubMed-8454635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P46170; 1BNB.
InterPro; IPR001855; -.
Jefam; PF00711; Defensin_beta; 1.
Antiblictic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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21.9%;
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37.5%;
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27
35
4278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.9
Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CTVTALLGCSCKSKVC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AA;
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7
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P46159;
                                                                                                                                                                                                                                                                                                                                                                                                            Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD01_BOVIN
            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID DDT TO DD T TO DD TO DD
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Gentianales; Rubiaceae; Psychotria.
NCBI_TaxID=41680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     active, 31-residue cyclic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viola odorata (Sweet violet).

Bukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Malpighiales; Violaceae; Viola.

NCBI_TaxID=97441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Witherup K.M., Bogusky M.J., Anderson P.S., Ramjit H., Ransom R.W., Wood T., Sardana M.;
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         Pred. No. 4.6e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A3D8CA231098E7E7 CRC64;
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Pred. No. 5e+02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYCLOVIOLACIN 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYLA_PSYLO STANDARD; PRT; 31 AA. P56872; P82254; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) CYCLOPSYCHOTRIDE A (CPT).
                                                                                                                                                                                                                                                                                                                       30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHESIS, AND ANTIBACTERIAL ACTIVITY. MEDLINE-99362685; PubMed-10430870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cyclopsychotride A, a biologically isolated from Psychotria longipes."; J. N<sub>2</sub>t. Prod. 57:1619-1625(1994).
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95230294; PubMed=7714530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.48;
37.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AA; 3141 MW;
         42.9%;
                                  Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                  38
                                                                                                                                     4 VVVLGGGISGDSLC 17
                                                                                                  25 VVAIPGNASMDAVC
         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                CYO1_VIOOD
P82230;
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TO CYLA_PSYLO
AC P56872
DT 30-MAY.
DT 30-MAY.
DE 30-MAY
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CYO1_VIOOD
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Gaps

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Indels

Length 38;

E.COLI ML35

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Gaps

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Length 31; 8; Indels

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(Rel. 34, (Rel. 34, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLVDIPIPANDDAI 14
                                                   Lectin, Glycoprotein
NON_TER 24
SEQUENCE 24 AA; 26
                                                                                                       Query Match
Best Local Similarity
Matches 6; Consery
                                                                                                                                                 6 TFSNTTSSTD 15
                                                                                                                                                                     5 SFSSTKFSTD 14
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=35137
                                                                                                                                                                                                                                                                                                                                                                STRAIN-CCMP 593
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01-NOV-1997 (
CHLOROPLAST 3
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01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                           Chloroplast.
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P50982;
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Q40606;
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SEQUENCE
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CXA1_CONER
ID CXA1_C
AC P50982
DT 01-0CT
DT 01-0CT
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RR2_OCHNE
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1-- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL COMPOUNDS, INCLUDING A METYRARONE BASED CLASS OF INSECTICIDES, TO THE RESPECTIVE ALCOHOL METABOLITES.
                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ANDROSTERONE + NAD(P)(+) = S-ALPHA -NADROSTENE-3,17-DIONE + NAD(P)H. SUBGELLULAR LOCATION: CYTOPLASHIC SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-RUG-1991 (Rel. 17, Last annotation update)
LECTIN (FRAGMENT).
Crotalaria juncea (Sunn hemp).
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eucloctyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Crotalaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.50) (3-ALPHA-HSD)
(HYDROXYPROSTAGLANDIN DEHYDROGENASE) (HSD29) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                         INVOLVED IN COFACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       9506860D070A7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 1; I
Pred. No. 4.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AA
                                                     15 AA
FASCHTNGGICLPNR-----CPGHMIQIGIC
                                                                                                                                                                                                                                                                                                                                  PS00061; ADH_SHORT; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                     PRT;
                                                                                                                                                                              MEDLINE-97100200; PubMed-8944761;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                       15 AA; 1315 MW;
                                                                                                                                    Bacteria; Proteobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        >15
                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|| |:||
2 VIAITGSAS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 VVAIPGNAS 33
                                                                                                                                                                                                                                                                                                                                (SDR) FAMILY
                                                                                                                             Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase;
                                                                                                                                              NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Seed;
                                                   DIDH_PSESP
P80701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEC_CROJU
P16352;
                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                              RESULT 11
DIDH_PSESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
LEC_CROJU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huss V.A.R., Tietze A.C., Julius C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                 Score 29; DB 1; Length 24;
Pred. No. 7.3e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Haptophyceae; Isochrysidales; Ochrosphaera
                                                                                                                                                                         80704D8CD9F9BB6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 AA; 3640 MW; 2039BA0FB5710655 CRC64;
InterPro; IPR000985; -.
InterPro; IPR001220; -.
Pfam; PF000139; lectin_legB; 1.
PROSITE; PS003007; LECTIN_LEGUME_BETA; PARTIAL.
PROSITE; PS00308; LECTIN_LEGUME_ALPHA; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
30S RIBOSOMAL PROTEIN S2 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 1;
Pred. No. 1e+03;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001865; -.
Pfam; PF00318; Ribosomal_S2; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00963; RIBOSOMAL_S<_Ribosomal protein; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X99078; CAA67534.1; -.
                                                                                                                                                                                                                                                   13.4%;
                                                                                                                                                                         24 AA; 2614 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ochrosphaera neapolitana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0
                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                           Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Comp. Endocrinol. 83:227-232(1991).
-!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
                                                                                            -i- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS (N RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION. - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PIR: $69348; GCFLE.
PIR: $61135; A61135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Platichthys.
NCBI_TaxID=8260, 8241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Navarro I., Gutierrez J., Caixach J., Rivera J., Planas J.; "Isolation and primary structure of glucagon from the endocrine pancreas of Thunnus obesus.";
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MEDLINE-87219793; PubMed-3556313;
Conlon J.M., Davis M.S., Thim L.;
Primary Structure of insulin and glucagon from the flounder (Platichlys fleaus).";
Gen. Comp. Endocrinol. 66:203-209(1987).
          Conus ermineus (Atlantic fish-hunting cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                      Score 28; DB 1; Length 18;
Pred. No. 7.4e+02;
1; Mismatches 5; Indels
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60A61A6C427A6B5E CRC64;
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01-NOV-1991 (Rel. 20, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
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MEDLINE=92009094; PubMed=1916209;
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18
2082 MW;
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Best Local Similarity
Matches 5; Conserv
ALPHA-CONOTOXIN EI
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                                              NCBI_TaxID=55423;
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P23062;
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GLUC_PLAFE
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Pred. No. 1.2e+03;
Pred. no. 1.2e+03;
Indels
HSSP; P01274; 1GCN.
InterPro; IPR000532; -.
Pfam; PF00123; hormone2; 1.
PRINTS; PR00275; GLUCAGON.
PROSITE; P$00206; GLUCAGON; 1.
Glucagon family; Hormone.
SEQUENCE 29 AA; 3508 MW; 77D5943208662E52 CRC64;
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Job time: 166 sec
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75.0%;
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076030 homo saplen 09hf27 cryptococcu 09ngy1 homo saplen 09f216 spinacia ol 09f26 spinacia ol 005602 pseudomonas 078505 human immun 035630 mus musculu 091145 hepatitis c 099214 aegilops sq 098746 streptomyce 016368 homo saplen 013254 homo saplen 013254 homo saplen 010486 human immun 09qqt2 tanapox vir 09ur51 filobasidie 09wul mus musculu 07847 human papil 09fa0 human papil 09143 human papil 04143 human immun 089539 human immun 010485 human immun

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Title: Perfect score:

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protein

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Run on:

Scoring table:

Searched:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                 Komata T., Tsuchiya N., Matsushita M., Tokunaga K.; "New poliymorphism within the extracellular region of TNFR2."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 121; DB 4; Length 30;
Pred. No. 4e-10;
0; Mismatches 0; Indels
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3183 MW; 942C00239B909DF5 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CD8 BETA CHAIN ISOFORM S BETAS (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 (FRACMENT).
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Q77939
Q97630
Q99627
Q90072N
Q9972N
Q9972N
Q9972
Q78505
Q9563
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Q9WUU1
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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Homo sapiens (Human).
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                  Receptor.
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Qyudb4 homo sapien
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Q70294 human immun
Q70351 human immun
Q70351 human immun
Q70351 human immun
Q92x49 bacteriopha
P79330 bos taurus
Q9iexl cotton leaf
Q9qys rattus sp.
Q9psz xylella fas
Q9psz xylella fas
Q9dusz homo sapien
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09mawa pongon pygma
09hf26 cryptococcu
09hdp1 filobasidie
09ndp0 cryptococcu
09trd4 oryctolagus
09n310 caenorhabdi
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216
1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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SEQUENCE FROM N.A. MEDLINE-94338597; PubMed-8060542; MEDLINE-94338597; PubMed-8060542; Bobkov A.F., Garaew M., Rzhaninova A., Kaleebu P., Pitman R., Weber J.N., Chelngsong-Popov R.; Weber J.N., Chelngsong-Popov R.; Molecular epidemiology of HIV-1 in the former Soviet Union: analysis implemores and their correlation with epidemiologic data."; AIDS 8:619-624(1994).
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Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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MEDLINE-93329178; PubMed-8335967;
Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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Pred. No. 3.7e+02;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
                                                                                                                                 Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
35 AA
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  PRT;
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J. Infect. Dis. 168:292-297(1993).
BMBL; U10706; AAA19263.1;
InterPro; IPR000777;
Pfam; PF00516; GP120; 1.
Envelope protein.
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47.6%;
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Matches 10;
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MEDLINE-94338597; PubMed-8060542;
Bobkov A.F., Garaev M., Rzhaninova A., Kaleebu P., Pitman R.,
Weber J.N., Cheingsong-Popov R.;
"Molecular epiddemiology of HIV-1 in the former Soviet Union: analysis
of env V3 sequences and their correlation with epidemiologic data.";
AIDS 8:619-624(1994).
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SEQUENCE FROM N.A.
MEDLINE-93170376; PubMed-8436166;
DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
"Transcriptional diversity at the duplicated human CD8 beta loci.";
Eur. J. Immunol. 23:320-326(1993).
Eur. J. Immunol. 23:320-326(1993).
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Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.7e+02;
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InterPro; IPR000777; -.
Pfam; PF00516; GP120; 1.
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Local Similarity
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Matches 10; Conservative
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"Identification of human immunodeficiency virus type 1 subtypes and their distribution in the Commonwealth of Independent States (Former Soviet Union) by serologic V3 peptide-binding assays and V3 sequence
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE-93329178; PubMed-8335967;
Cheingsong-Popov R., Bobkov A.F., Garaev M., Kaleebu P., Callow D.,
Rzhaninova A., Saukhat S.R., Burdajev N.P., Kolomijets N.D.,
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                                                                                                                                                                                                                                                                                                                   Length 35;
                                                                                                                                                                                                                                                                                                                                                            9; Indels
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NON_TER 35 35
SEQUENCE 35 AA; 3852 MW; 5C5827FCBD5DB873 CRC64;
                                                                                                                                                                                                                                                5C5827FCBD5DB873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN, V3 REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                            16.7%; Score 36; DB 14;
11arity 47.6%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 9:
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EMBL, U10764; AAA19329.1; -.
Pfam; PP00516; GP120; 1.
Envelope protein.
                                                                                     J. Infect. Dis. 168:292-297(1993).
BERL: UIO707, AAA19264.1; -.
INTERPL: PF00516; GP120; 1.
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35
3852 MW;
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hes 10; Conservative
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35 AA;
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                               Envelope protein.
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NON_TER
SEQUENCE
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TISSUE-CARTILAGE PROTEOGLYCAN;

MEDLINE-97079270; Pubmed-8921002;

Fulop C., CS-Szabo G., Glant T.T.;

"Species-specific alternalive splicing of the epidermal growth factor-like domain 1 of cartilage aggrecan.";

Biochem. J. 319:935-940(1996).

EMBL; L29486; AAB48067.1; -.

NON_TER

SEQUENCE 36 AA; 3614 MW; 9F6C32F15D3BC9DB CRC64;
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Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                               "Characterization of ARI coliphage specific to enterohemorrhagic Escherichia coli 0157:H7."; Escherichia coli 0157:H7."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF022930; ADDJJ56.1; -
                                                                                                                                                                                     dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
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                                                                                                                                                                                                                                                                                                            Syu W.J., Ding H.C., Seah J.N., Wu K.M., Yu S.L., Tam M.F.,
Chang Y.C.;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
AGGRECAN EPIDETMAL GROWTH FACTOR-LIKE DOMAIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 AA; 2830 MW; 5875E0CFBB665934 CRC64;
                                             01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PUTATIVE VERTEX HEAD SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 34.5; DB 6; 34.8%; Pred. No. 6.1e+02; tive 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.2%; Score 35; DB 9; 50.0%; Pred. No. 3.8e+02; tive 2; Mismatches 4
26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Best Local Similarity 50.0
Matches 10; Conservative
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  PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                             Bacteriophage AR1
                                                                                                                                                                                                                                  NCBI_TaxID=66711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9913;
                                                                                                                                                                                     Viruses; dsDNA v
T4-like phages.
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Q9IEX1
ID Q91
AC Q93
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SITALINE-2035517; PubbMed-10910347;

SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

Alvarenga R., Alves L.M.C., Arryda J.E., Bata G.S., Baptista C.S.,

Barros M.H., Bonaccorsi E.D., Bordin S., Baye G.S., Bartines M.R.S.,

Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

Colauto N.B., Colombo C., Costa M.C.R., Costa M.C.R., Costa M.C.R.,

Coutinho L.L., Cristofani M., Dias-Netc E., Docena C., El-Dorry H.,

Raga J.S., Franco M.C., Franco M.C., Frone M., Fulla L.R.,

A Garnier M., Goldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P.,

R. Hop.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

A Garnier M., Goldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P.,

A Garnier M., Mardins E.E., Laigret F., Lambais M.R., Leite L.C.C.,

Lemos B.C., Lopes C.R., Lopes C.R., Machado J.A.,

A Marques M.V., Martins E.A.L., Martins A.A., A de Oliveira R.C., Jenimieria J.C., Savasaki H.E.,

A Gasjiveira J.F., Silveira M., Verjovski-Almeida S., Vettore A.L.,

A Gago M.A., Zaro M.A., Verjovski-Almeida S.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
AMGX PROTEIN (FRAGMENT).
HOMO saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
Babi. AE004018; AAF84790.1; -.
Hypothetical protein.
SEQUENCE 39 AA: 4501 MW; E085D64BE286D612 CRC64;
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MEDLINE-95322983; PubMed-7599636;
Lench N.J., Winter G.B.;
"Characterisation of molecular defects in X-linked amelogenesis
                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 2; Length 39;
Pred. No. 1.1e+03;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                              01-MAR-2001 (TrEMBLrel. 16, HYPOTHETICAL PROTEIN XF1988.
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Hum. Mutat. 5:251-259(1995).
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Best Local Similarity
                                                                                                                     Xylella fastidiosa
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=2371;
                                                                                                                                                                                  Xylella
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Q9UD12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
OLIGODENDROCYTE-SPECIFIC UDP-GALACTOSE:CERAMIDE GALACTOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                               Sanz A.I., Fraile A., Garcia-Arenal F., Zhou X., Robinson D.J.,
Khalid S., Butt T., Harrison B.D.;
"Multiple infection, recombination and genome relationships among
begomovirus isolates found in cotton and other plants in Pakistan.";
D. Gen. Virol. 81:839-1849(2000).
EMBL: AJ270854; CAB97069.1;
InterPro: IPR002488;
InterPro: IPR002488;
Probom: PP001492; Gemini_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 6.6e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 11; Length 15; Pred. No. 4.2e+02; 11 Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F3121B92E34ED31E CRC64;
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E 15 AA; 1657 MW; 84474749A06BFFCC CRC64;
   Created)
Last sequence update)
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                                                                                                                                                                      Viruses; ssDNA viruses; Geminiviridae; Begomovirus NCBI_TaxID=53010;
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Q9PBZ7; 0
01-OCT-20Q0 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                            STRAIN=P12-IR;
MEDLINE=20318672; PubMed=10859391;
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Best Local Similarity 41.7°,
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                      01-MAR-2001 (TrEMBLrel. AC4 PROTEIN (FRAGMENT).
                                                                                                                                                 cotton leaf curl virus.
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15 NSNAGTTVLRPH 26
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2 PGIFXSTTS 10
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01-JUN-2000
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ID 09PBZ7
AC 09PBZ7;
DT 01-0CT-:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodman M.; .
    "The place of Callimico goeldii in the Callitrichine phylogenetic tree: evidence from von Willebrand factor gene intron II sequences."; Mol. Phylogenet. Evol. 13:392-404(1999).

EMBL; AF092833; AAF77601.1;
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=85755;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
VON WILLEBRAND FACTOR (FRAGMENT).
Pongo pygmacus (Oranqutan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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MEDLINE-20072937; Pubmed-10603266;
Chaves R., Sampaio I., Schneider M.P., Schneider H., Page S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 32; DB 14; Length 34; 38.5%; Pred. No. 1.3e+03; tive 4; Mismatches 4; Indels
                                          Query Match 14.8%; Score 32; DB 4; Length 33; Best Local Similarity 26.9%; Pred. No. 1.3e+03; Matches 7; Conservative 4; Mismatches 15; Indels
     3681 MW; D131F784BD7D8C93 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
7.7 KDA PROFEIN.
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Matches 5; Conservative
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Best Local Similarity 33.3
Matches 8; Conservative
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16 TTLNHDMAKPHYL 28
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    33 AA;
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Chaturvedi S., Rodeghier B., Fan J., McClelland C.M., Wickes B.L., Chaturvedi V.;
Chaturvedi V.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226946; AAG41335.1;
NON_TER 1
SSEQUENCE 33 AA; 3470 MW; 0795B64C46ED4CE6 CRC64;
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                                                                                                                                                                                                                                                                                                                           Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Tremellales;
Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHEROMONE PRECURSOR MATALPHA (FRAGMENT).
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                                                                                                                                              33 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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PRELIMINARY;
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July 13, 2001, 16:58:40 ; Search time 19.99 Seconds (without alignments) 118.276 Million cell updates/sec
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1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Costant and variab	Human 5' EST secre	Human secreted pep	P. pastoris lysyl	P. pastoris lysyl	Human 5' EST relat	Adenovirus hexon p	Human secreted pro	Yada homologous pe	Human secreted pro	NF-AT transcriptio	
SUMMARIES	AAW95323	AAY12433	AAB37394	AAY51961	AAY51973	AAY64941	AAY24434	AAB44864	AAB51542	AAW73416	AAR70346	
DB	20	20	21	21	21	21	20	21	21	20	16	
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% Query Match	21.3	21.3	19.4	19.0	19.0	18.5	18.1	17.4	17.1	17.1	16.7	
Score	46	46	42	41	41	40	39	37.5	37	37	36	
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AAY96558 AAB66490 AAW65481 AAW67402 AAW67476 AAW65476 AAW65476 AAW65470 AAX02252 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX06092 AAX01310 AAX13109 AAX10109 AAX10109 AAX10109 AAX10109 AAX10109 AAX101	17 AA. sequence of C ementary body sponse; infec; ; autofmmune; lant.
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human secreted proteins, and encode the proteins given in AAY12561 to human secreted proteins, and encode the proteins given in AAY12561 to AAY12514, respectively. The proteins given represent the signal peptide and an N-terminal fragmen of a secreted protein. The nucleic acid sequences can be used for producins secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, call protificration/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ligand activity, anti-inflammatory thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, den for activity or other activity. The products can be used in forensic, gene therapy and chromosome mapping promoter. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                  New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted peptide #32 encoded by cDNA #47.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                         WPI; 1999-153778/13.
                                                                                                                                                                                                                                    N-PSDB; AAX41266
                                                                                                      (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200058335-A1.
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                     01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1999;
22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000
                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB37394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB37394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against recombinant major outer membrane protein (MOMP), and for DNA amplification assays for chlamydial genes, are used to diagnose disease, e.g. autofinmune disease, an inflammatory disease or a disease that occurs in an immuno-compromised individual, associated with Chlamydia infection. The kits are used to detect chlamydial elementary bodies in a sample. They are also used to monitor and/or modify the course of therapy in a patient. The treatment reduces the acellular load of infectious Ebstein Barr virus. The method is also used to treat porphyria, by reducing the number of elementary bodies and applying a drug, e.g. cimetidine, and antioxidants, to reduce the adverse effects associated with porphyria. Sequences AMM95120 to AAM95121 represent constant and variable domain sequences of various Chlamydia species.
                                                                                                                                                                                                                                                                                                                                The invention relates to the diagnosis and management of infections by Chlamydia species. The invention provides a composition that comprises at least two agents, where each of the agents is effective against a different phase of the chlamydial life cycle. The agents are selected from: (a) agents targetted against cryptic phase of chlamydial life cycle; (b) agents targetted against elementary body phase of chlamydial life cycle; (c) agents targetted against replicating phase of chlamydial life cycle; (d) probenicid, and (e) antiporphyric acid. The composition is used to elicit a protective immune response to Chlamydia infection in an animal or human and is applied until the animal or human tests material infected with Chlamydia. Diagnostic kits for antibody assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forensic; gene therapy; chromosome mapping; signal peptide; upstream regularory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                    Composition with two agents effective against different stages of chlamydial life cycle - comprises agent targetted against cryptic phase, against elementary body phase, against replicating phase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 20; Length 17;
Pred. No. 9.6;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 5' EST secreted protein SEQ ID NO:464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY12433 standard; Protein; 38 AA
                                                                                                                                                                                                                                                                                     Claim 4; Fig 3; 138pp; English.
                                                                                                                                                                                                                                    probenicid and antiporphyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.3%;
                                                   Stratton CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 64.3
(UYVA-) UNIV VANDERBILT.
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                                                                                                   WPI; 1999-059653/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 AA;
                                                   Mitchell WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9906548-A2
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AAY12433 RESULT

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Gaps

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ore 46; DB 20; Length 38; ed. No. 23; Mismatches 12; Indels

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Friedrich T,
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                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY51973;
                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                        AAY51973
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                                                                                                                                                      Sequences AAB37348-B37394 represent the amino acid sequences of 47 human secreted proteins encoded by the genes AAC68081-C68127. The genes and proteins are useful for preventing, ameliocathing or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                                                                                                                                                                                                                                      (b) Immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colifis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                            encoding human secreted proteins, used to treat, prevent, diagnose conditions such as cancer, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 21; Length 36;
Pred. No. 75;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klingler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. pastoris lysyl oxidase peptide fragment #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Friedrich T, Bewert W, Lueddecke E,
                                         Komatsoulis G;
                                                                                                                                      Claim 11; Page 366; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY51961 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                            19.4%;
         (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
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                                                                                                                 diseases e.g. arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                     SSTDICRPHQICNVVAI 28
                                                                                                                                                                                                                                                                                                                                                                                                                                   13 sstracapricenlily 29
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                             lepsy; and (f) infect: parasitic infections
                                        Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserv
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                                                            WPI; 2000-611702/58
N-PSDB; AAC68127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia pastoris
                                                                                            acids
                                                                                                                                                                                                                                                                                                                                             36
                                                                                                       ameliorate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19840069-A1
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                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                           Nucleic
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ID AAY5
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an active substance, where the active substance is surrounded by at least one layer consisting of a protein that is cross-linked by an enzyme chosen from the group of lipoxygenase, protein disulfide isomerase, phenol oxidase and peroxidase, lysyl oxidase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases. Enzymes chosen from lipoxygenase, protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases is protein disulfide reductase, tyrosine oxidase or sulfhydryl oxidases, especially lysyl oxidase are useful for formulation of preparations of active substances. The method of the invention is preparations are useful as food additives or fodder or as pharmaceuticals. AAYS1962 represent fragments of the Pichia pastoris lysyl oxidase which are used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lysyl oxidase; lipoxygenase; protein disulfide isomerase; phenol oxidase; peroxidase; protein disulfide reductase; tyrosine oxidase; food; sulfhydryl oxidase; animal feed.
Manufacture of active preparations comprises cross linking a protein, which surrounds the active substance with an enzyme, especially a novel lysyl oxidase from Pichia pastoris
                                                                                                                                                                                              This invention describes a novel method to manufacture a preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method where an enzyme (I) selected from lipoxygenases, protein disulfide isomerases, phenol oxidases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of specified enzymes, especially lysyl oxidase, as protein consolithing agents for formulating compositions containing active incredients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 17;
45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klingler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P. pastoris lysyl oxidase fragment #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51973 standard; peptide; 17 AA.
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                                                                                                                              Claim 17; Page 17; 22pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-272257/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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AAY6438 represent the EST-related proteins. AAY64631 to
AAX6438 represent the EST-related proteins. AAX6451 to
AAX13052. The 5 ESTS can be used for producing secreted human gene
products. They can be used for producing secreted human gene
products. They can be used to identify and isolate 5 'untranslated
regions (UTRs) and upstream regulatory regions which control the
location, development stage, rate, and quantity of protein synthesis, as
well as stability of mRNA. The ESTs are also useful as probes for
chromosome mapping, and to obtain full length cDNA clones. The ESTs can
also be used in forensic procedures to identify individuals, or in
diagnostic procedures to identify individuals, or in
gene therapy protocols. The nucleic acids encoding signal peptides can be
used for directing extracellular secretion of a polypeptide or the
peroxidases, lysyl oxidases, protein disulfide reductases, tyrosine oxidases or sulfiydryl oxidases is used to formulate compositions containing active ingredients. (I) is useful for crosslinking protein layers surrounding active ingredients in food, animal feed and pharmaceutical products. The compositions can be formulated without using chemical crosslinking agents. AAY51963-Y51974 represent fragments of the Pichia pastoris lysyl oxidase protein which is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedum
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                                                                                                                                                                                                      DB 21; Length 17;
                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 5' EST related polypeptide SEQ ID NO:1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                     Score 41; DB;
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY64941 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 687; 837pp; English.
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                                                                                                                                                                                                                     19.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-IB00712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                   Query Match 19.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-038446/03.
N-PSDB; AAZ42555.
                                                                                                                                                                                                                                                                                         1 PCAPGTFSNT 10
                                                                                                                                                                                                                                                                                                                            7 pcapgvvynt 16
                                                                                                                                                                 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY64941;
                                                                                                                                                                 Sequence
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AAY64941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an adenoviral capsid protein comprising a heterologous ligand, where the ligand facilitates binding of the adenovirus to a target cell. The adenoviral vector is used to transfer a transgene to a target cell. The heterologous ligand in the adenoviral capsid protein (especially a fibre or hexon protein or protein IX) adenoviral vector to the target cell. In particular, the adenoviral vector can be used to transfer the human cystic fibrosis transmembrane conductance regulator protein gene to the respiratory epithelium of test animals. The modified adenoviral capsid proteins improve and/or alter the infectious capability of the vector. The present sequence represents an adenovirus haxon protein heterologous ligand used in an example from the present invention.
                    be useful in
insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42244 and AAZ464644 to AAZ4650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenovirus; RGD sequence; adenoviral vector; capsid protein; ligand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenoviral vectors with modified capsid proteins for improved infectious capabilities
                                                                                                                                                          Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26;
                                                                                                                                           Score 40; DB 21; Length 20
Pred, No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 20; L/Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      Adenovirus hexon protein heterologous ligand #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romanczuk H;
                                                                                                                                                                                                                                                                                                                             AAY24434 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1A; 59pp; English.
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                                                                                                                                                          18.5%;
41.2%;
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                                                                                                                                                                                                                     2 CAPGTFSNTTSSTDICR 18
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                                                                                                                                                                                         Conservative
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                                                                                                                                             Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mastadenovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection
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                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative disorders, cardiovascular disorders such as arterioarterial fistula, arrhythmias, arteriosclerosis, coronary thrombosis, organ regeneration, cancer, necvascular glaucoma, diabetic retinopathy, rheumatoid arthritis, psoriasis, diseases associated with increased apoptosis that include acquired immunodeficiency syndrome (AIDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes a novel isolated polypeptide (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; antiarteriosclerotic; antiinflammatory; nootropic;
neuroprotective; antidiabetic; tranguiliser; vulnerary; antibacterial;
antipsoriatic; antiarrhythmic; antirheumatic; cardiant; anti-HIV;
autofimmune disorder; allergic condition; cardiovascular disorder;
cancer; neurological disease; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel 49 human secreted proteins useful for diagnosis, prevention and treatment of disorders including neurological, cell proliferative, cardiovascular, and autoimmune/inflammatory disorders and microbial
                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; cytostatic; antiarthritic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                  Human secreted protein encoded by gene 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 373-374; 405pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis G;
                                                                                                                                                                                   AAB44864 standard; Protein; 34 AA.
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99US-0138597.
99US-0168666.
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                                            ||||||| : |: ||| snttssdqlaspyshprvv 19
                                                                                                                                                                                                                                                                                   (first entry)
                      SNTTSSTDICRPHOICNVV
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11-JUN-1999;
03-DEC-1999;
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                                                                                                                                                                                                                                                                              09-FEB-2001
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                                                                                                                                       RESULT
AAB44864
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                                                                                             including cosmetic plastic surgery, to treat fibrosis, reperfusion injury or systemic cytokine damage, to stimulate chondrocyte growth, to prevent skin aging due to subburn, to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression, memory, stress and for accelerating wound healing. (I), (II) and/or their agonist or antagonist are useful as food additives or preservatives to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamin, mineral or other nutritional components. (I) is useful in forensic biology for detecting bNA sequences and as diagnostic probes for detecting the presence of specific mRNA in a particular cell type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to peptides AAB51512 - AAB51537 which represent conserved proteobacterial extracellular domains. Sequences AAB51518 represent peptides homologous to YadA, a yersinia adhesin which is an important virulence determinant of the Yersinia species. The invention includes an antibody which binds to the proteobacterial extracellular peptides, and an immunogenic composition containing the antibody used as a vaccine to prevent infection by a proteobacteria. The polypeptides and antibodies are useful in the treatment and prevention of proteobacterial infections. The polypeptides can also be used to identify compounds which antagonize the binding of a bacterial adhesion to its ligand. The host cell can be used to produce
neurological diseases such as Parkinson's disease, viral, bacterial, fungal or parasitic diseases. They are also used to repair, replace or protect tissue damage by congenital defects, to treat trauma, in surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated polypeptide conserved in proteobacterial extracellular domains used in the treatment and prevention of bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesin; proteobacterial infection prevention; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37.5; DB 21;
Pred. No. 2.8e+02;
6; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%;
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13 tilniattstlck-hqvc 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200061165-A1.
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RESULT 1
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the polypeptides in a suitable culture system. The composition can be used to vaccinate a patient against a proteobacterial infection.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders or blood disorders
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                                                                                                                                                 Score 37; DB 21; Length 22;
Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein encoded by Gene No. 20.
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                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAW73416 standard; Protein; 23 AA
                                                                                                                                            17.1%;
50.0%;
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97US-0048093.
97US-0048101.
97US-0048190.
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97US-0050935.
97US-0056250.
97US-0056293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1999 (first entry)
                                                                                                                                                                        Best Local Similarity 50.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-070209/06
                                                                          A.
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
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29-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW73416;
                                                                          Sequence
                                                                                                                                                 Query Match
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SSXS
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Gene No. 20. This sequence represents a human secreted protein, and is expressed ubiquitously, including T-cells and amygdala. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions

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can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and ADDS. The polypeptides are also useful for identifying
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NF-AT peptide fragment; transcription complex; autoimmune diseases; immunomodulatory agents; T-cell related conditions; lymphocytic leukaemia; transplant rejection reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides can be used as immunomodulatory agents, useful in the diagnosis and treatment of T-cell related conditions, e.g autoimmune diseases, lymphocytic leukaemias and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA and polypeptide(s) encoding the transcription complex NF-AT
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70345-R70356 are peptide fragments of the human NF-AT transcription complex, a NF-AT polypeptide containing at least one of these peptide fragments is claimed. The claimed NF-AT
                                                                                                                                                                                                                                                                           Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for use as immunomodulatory agents in the diagnosis and treatment of T-cell related conditions
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                       ore 37; DB 20; L
ed. No. 2.1e+02;
Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF-AT transcription complex peptide fragment.
                                                                                                                                                                                                                                                                         Score 37;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%; Score 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR70346 standard; Peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 64; 84pp; English.
                                                                                                                                                                                                                                                                           17.1%;
43.8%;
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94US-0260174
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                                                                                                                                                                                   their binding partners
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Best Local Similarity
Matches 7; Conserv
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13-JUN-1994;
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                                                                                                                                                                                                                        Sequence
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Screening assay for identifying modulators of translocation of nucl factor of activated T lymphocytes across nuclear membrane of cell, treating with nuclear factor of activated T lymphocyte polypeptide
                                                                 Human; nuclear factor of activated T lymphocytes; NF-AT; NF-AT cytoplasmic component; NF-ATC; NF-AT translocation; nuclear localisation sequence; NLS; SRR.
                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND STANFORD JUNIOR,
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 23; 99pp;
                                          Human NF-AT peptide
                                                                                                                                                                                                                                                                                                                        WPI; 2001-122328/13.
                                                                                                                        Homo sapiens
                                                                                                                                                US6171781-B1
                                                                                                                                                                                                                                                                                              Crabtree GR,
                                                                                                                                                                                                                              20-SEP-1993;
                                                                                                                                                                                                                                          13-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel method for preventing and/or reducing cardiac hypertrophy in a patient, comprises administering an NF-AT (nuclear factor of activated T cells) antagonist to decrease the biological activity of NF-AT in myocardial tissue (therefore preventing and/or reducing the level of cardiac hypertrophy). The antagonists may decrease the transcriptional activity, nuclear translocation or dephosphorylation of NF-AT, inhibit binding of calcineurin to NF-AT, stimulate phosphorylation of NF-AT (e.g. binding of calcineurin to NF-AT, stimulate phosphorylation of NF-AT (e.g. antagonist is an antagonist of NF-ATC) (also known as NF-AT4) and not NF-ATC), NF-ATC2 and NF-ATC3 (also known as NF-AT4). The method is used for preventing and/or reducing cardiac hypertrophy in a patient suffering from congestive heart disease (claimed) and for preventing other growth
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                Gaps
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                                                                                                                                                                                                                                       NF-ATC1; cardiac hypertrophy; nuclear factor of activated T cells; antagonist; congestive heart disease; cardiant; antigen.
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Pred. No. 2.8e+02;
; Mismatches 2; Indels
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating cardiac hypertrophy using NF-AT antagonists in patients suffering from congestive heart disease
 Pred. No. 2.8e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                               Human NF-ATcl antigenic peptide 7.
                                                                                                                                  AAY96558 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac and vascular tissue.
46.78;
                                                                                                                                                                                                                                                                                                                                                             99WO-US27862
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                                                                                                                                                                                     12-SEP-2000 (first entry)
               Conservative
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                                         DICRPHQICNVVAIP 29
                                                                6 dlckpnsl--vveip 18
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Best Local Similarity
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Best Loeal Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Crabtree GR,
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             23-NOV-1999;
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                                                                                                                                                           AAY96558;
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nuclear ell, by

English.

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Northrop JP,

93US-0124981. 98US-0049691

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The present sequence is given in a specification relating to a method for identifying a compound which modulates translocation of a nuclear factor of activated T lymphocytes (NF-AT) polypeptide across the nuclear membrane of a cell. The method involves binding the compound to the NF-AT polypeptide. The method is useful for identifying compounds which modulate nuclear translocation of NF-AT present in the cytoplasm and/or in the nucleus of the cell and for identifying agents that modulate phosphorylation/dephosphorylation of NF-AT.
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annexin V; hepatitis B surface antigen; immunogen; vaccine; hepatitis delta virus; infection; HBsAg.
                                                                                                                                                                                                                                                Length 22;
                                                                                                                                                                                                                                            16.7%; Score 36; DB 22; Length 22
46.7%; Pred. No. 2.8e+02;
.ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B surface antigen derived peptide (IGP 1082).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW65481 standard; peptide; 23 AA.
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                                                                                                                                                                                                                                                                                                                             15 DICRPHQICNVVAIP
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Best Local Similarity
Matches 7; Conserv
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Hepatitis b virus.
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AAB66490 standard; Peptide; 22 AA.

RESULT 13

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AAB66490

AAB66490 ID AAB6 XX AC AAB6

15 DICRPHQICNVVAIP 29 |:|:|: || || 6 dlckpnsl--vveip 18

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haemagglutinin-neuraminidase (HN) protein of the paramyxoviridae. The specification describes 3-D models identifying a proteinaceous substance comprising at least one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. The antigenic sites can be used to produce vaccines, to detect the viruses, and to select the immunodominant
                                                                                                                            Isolated proteinaceous substance - comprising at least one virus epitope derived from an attachment protein of a paramyxovirus
                                                                                                                                                                                                                         AAW97452-571 represent antigenic sites derived from the
                    (DIER-) STICHTING INST DIERHOUDERLY EN DIERGEZON
                                                                                                                                                                                   Disclosure; Page 46; 63pp; English.
                                                    Langedijk JPM, Van Oirschot JT;
                                                                                          WPI; 1999-120896/10.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                        The invention relates to an immunogenic peptide derived from hepatitis B surface antigen (HBSAg) which competes with the hepatitis B surface antigen/annexin V interaction or which binds a compound or antibody competing with the hepatitis B surface antigen/annexin V interaction.

Also claimed are: (1) a combination of the immunogenic peptide and a negatively charged phospholipid; (2) a peptide composition comprising the immunogenic peptide; (3) a vaccine comprising the immunogenic peptide (4) antibodies which specifically bind to the peptide and inhibit binding of HBSAg to annexin V, and (5) a therapeutic composition comprising as an active substance the antibodies of (4).

The vaccine of (3), and the therapeutic composition of (5), can be used as an innoculum to vaccinate humans against an infection with hepatitis and/or hepatitis delta virus. The immunogenic peptide can be used in a method to detect antibodies which are capable of competing with the hepatitis B and/or hepatitis Delta virus surface antigen/annexin V interaction. The immunogenic peptide can also be used to screen for drugs which block the binding between annexin V and the peptide, and as a therapeutic to treat humans infected with hepatitis B virus and/or hepatitis Delta virus. The present sequence represents one of the peptide fragments derived from HBSAG which were synthesised to map the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                    Immunogenic polypeptide from hepatitis B surface antigen - useful
in, e.g. vaccine against hepatitis B virus or hepatitis delta virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.7%; Score 36; DB 19; Length 23; Best Local Similarity 37.0%; Pred. No. 2.9e+02; Matches 10; Conservative 4; Mismatches 7; Indels
                                                                                                                              Yap S;
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                                                                                                                              Maertens G,
                                                                                                                                                                                                                                                                          Example 3; Page 35; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97502 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annexin V-binding site on HBsAg
97WO-EP07268.
                                  97EP-0870103
96EP-0870164
                                                                                          (INNO-) INNOGENETICS NV.
                                                                                                                              De Meyer S, Depla E,
                                                                                                                                                                  WPI; 1998-388040/33
23-DEC-1997;
                                                    30-DEC-1996;
                                                                                                                                                                                                                                          Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae; virus epitope; attachment protein; vaccine; immunodominant epitope.

Bovine parainfluenza virus

WO9902695-A2 21-JAN-1999 98WO-NL00390 97EP-0202100

08-JUL-1998;

08-JUL-1997;

Antigenic site of HN protein loop beta-3L23.

19-MAY-1999 (first entry)

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                        Gaps
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        Length 23;
Search completed: July 13, 2001, 17:13:20 Job time: 880 sec
                       Conservative
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Ouery Match
Best Local Similarity
6; Conserve
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                                                     icnttgcpgktgrd
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23 AA;

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STREET: 635 Bryant
CITY: Palo Alto
STATE: California
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RESULT
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                                                                                                                                                                 July 13, 2001, 17:04:35; Search time 12.1 Seconds (without alignments) 64.929 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Patent No.
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-221-583-48
PCT-US55-04018-48
US-08-221-583-50
PCT-US55-04018-50
US-08-126-016-24
US-08-126-016-24
US-08-126-016-24
US-09-101-146-58
US-09-126-016-25
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US-08-221-583-46
PCT-US95-04018-45
US-08-221-583-44
PCT-US95-04018-44
PCT-US95-04018-49
US-08-221-583-49
US-08-221-583-47
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US-08-465-982-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-037-143-31
US-09-049-691-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                         193259 seqs, 20144635 residues
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                                                                                                                                                                                                                                                                             US-09-800-909-2_COPY_163_201
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 39
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                               Sequence Seq
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TWFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
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US-08-260-174-31
US-09-172-841-7
US-08-1942-481-7
US-08-787-091-9
US-08-59-556-7
PCT-US96-05262-12
US-08-444-005-19
US-08-444-005-19
US-08-444-005-19
US-08-451-472-7
US-08-451-472-7
US-08-290-448A-23
US-08-290-448A-23
US-08-290-448A-23
US-08-290-448A-23
US-08-290-448A-23
US-08-290-448A-23
US-08-390-448A-23
US-08-390-448A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION UNWARE: 33.208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 39; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 amino acids
      ; MOLECULE TYPE: protein US-08-050-319B-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5'CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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Gaps

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APPLICANT: Heavner, George A.

TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08221583
Patent No. 5486595
GENERAL INPORMATION:
APPLICANT: Heavner, George A.
TILLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
                                                                                                                                              35.6%; Score 77; DB 6; L 100.0%; Pred. No. 0.00026; ive 0; Mismatches 0;
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0.0012;
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Pred. No. 0.001
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIECATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELECHAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-00-221-583-45
Sequence 45, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
                                                                                                                                                   35.00,
100.0%; Fiv
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
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                                                                                                                                              Query Match 35.6
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 amino acids
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                            1 ICNVVAIPGNASMDA 15
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                                                                                                                                                                                                                                   22 ICNVVAIPGNASMDA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GTFSNTTSSTDICRP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                              ; LENGTH: 15
5395760-10
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US-08-221-583-46
                                            SEQ ID NO:10
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; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 39;
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APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
                                                                              Sequence 41, Application US/08465982

Patent No. 5863786

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
ITILE OF INVENTION: Medified human TNFalpha (Tumor TITLE OF INVENTION: Necrosis Factor alpha) Receptor NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 216; DB 2; 100.0%; Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ELING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBDINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                           ADDRESSEE: Reed & Robbins STREET: 635 Bryant Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-08-465-982-41
                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    94301
                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-RECEPTORS
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5395760-10
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Gaps

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01-APR-1994
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    FILING DATE:
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PCT-US95-04018-46
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 1; Length 15;
Pred. No. 0.0012;
0; Mismatches 1; Indels
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; Sequence 45, Application PC/TUS9504018
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Kruszynski, Marian
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Noodcock Washburn Kurtz Macklewicz 6
; ADDRESSEE: Noris
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CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/CDCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPASSION SYSTEM: PC-DOS/MS-DOS
SOFTMARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
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APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
93.3%;
                                                                                                                                                                                                                                                                       FILING DATE: US/01
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, Mark
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Best Local Similarity 93.3
Watches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-221-583-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNTTSSTDIARPHQI 15
                                                    CITY: Philauerr...
STATE: Pennsylvania
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                                                                                                                       19403
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Pred. No. 0.0012;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                      APPLIA
FILING DATE:
ATTORNEY/AGENT INFORMALL.
NAME: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0232
REFERENCE/DOCKET NUMBER: CCR-0232
TELECOMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAN: (215) 100: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
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TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: '46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.3
Best Local Similarity 93.3
Matches 14; Conservative
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Weber, Robert W.
               TITLE OF INVENTION:
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 APPLICANT:
                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                               Sequence 44, A59Dlication US/08221583
Facent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tunor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.9%; Score 71; DB 1; Length 15; 100.0%; Pred. No. 0.0016; Live 0; Mismatches 0; Indels
                                                                                                                                                     DB 5; Length 15;
                                                                                                                                                                       0.0012;
                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     Score 72;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
                                                                                                                                                     33.3%;
93.3%;
                   : 15 amino acids
amino acid
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
SEQUENCE CHARACTERISTICS
                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                      1 SNTTSSTDIARPHQI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-44
                                                                                                                                                                                                                              8 SNTTSSTDICRPHQI 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19403
                                                                                          PCT-US95-04018-46
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PCT-US95-04018-44
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Gaps
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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Pred. No. 0.0016;
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
Tumor Necrosis Factor Inhibitors 76
                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                           STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0; !
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide pcT-US95-04018-44
                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                            STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 APGTFSNTTSSTDI 16
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COUNTRY: USA
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Gaps
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GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5486595ris
STREET: One Liberty Place 46th Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                               Score 70; DB 5;
Pred. No. 0.0022;
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Pred. No. 0.0056;
                                                                                                                                                                                                                       0; Mismatches
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PCT-USS5-04018-47
Sequence 47, Application PC/TUS9504018
SERENAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marlan
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 47, Application US/08221583; Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNDABER: 33,229
REFERENCE/DOCKET UNDABER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                 32.4%;
92.9%;
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amino acid
                                              15 amino acids
                                                                                                                                                                                                                       13; Conservative
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      INFORMATION FOR SEQ ID NO:
                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-221-583-47
                                                                                                    peptide
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CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                    2 RPHQIANVVAIPGN 15
                                                                                                                                                                                                                                                              18 RPHQICNVVAIPGN 31
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                                                                                                                                                                                                     Best Local Similarity
                                                            amino acid
                                                                                    linear
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19403
                                                                                                  ; MOLECULE TYPE:
PCT-US95-04018-49
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                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-221-583-47
                                              LENGTH:
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                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Matches
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  SQFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Necrosis Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 1;
Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Liberty Place 46th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA
                                                                                                              NAME: DELUCA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
- APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/04018 FILING DATE:
                                        APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-04018-49; Sequence 49, Application PC/TUS9504018; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heavner, George A. APPLICANT: Kruszynski, Marian APPLICANT: Mervic, Miljenko APPLICANT: Weber, Robert W. TITLE OF INVENTION: Tumor Neci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,229
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                                                                                                                                                                                                                                                                                                                                                                                                                 32.4%;
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(215) 568-3439
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.4
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-221-583-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                          FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 RPHQICNVVAIPGN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RPHQIANVVAIPGN 15
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                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
SQFTWARE:
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SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Meber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 1;
Pred. No. 0.0075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                     CCOR-0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DeLuca, Mark
REGISTRATION UNMBER: 33,229
REFERENCE/DOCKET UNMBER: CCOR-0232
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US95/04018
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FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                        APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
PCT-US95-04018-48
PCT-US95-04018-48
Sequence 48, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.68;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US
                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (215) 568-3100
                                                                                                                                                                                                                                                                                                                    15 amino acids
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TDICRPHQICNVVAI 28
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COUNTRY: USA
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE MODGOCK Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STRYE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                            TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; D
                                                                                                                                            One Liberty Place 46th Floor
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Deluca, Mark
REGIETRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3400
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08221583; Patent No. 5486595; GENERAL INFORMATION:
APPLICANT: Mervic, Miljenko
                 APPLICANT: Weber, Robert W
TITLE OF INVENTION: Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide PCT-US95-04018-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TSSTDICRPHQICNV 25
                                                                                                                                          STREET: One Liberty
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                           19403
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Gaps

0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                        Run on:
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July 13, 2001, 17:38:33 ; Search time 13.26 Seconds (without alignments) 327.447 Million cell updates/sec

US-09-800-909-2\_COPY\_201\_257 Title:

1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

13308 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 57 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qallbladde	hypothetical prote		cenA protein (IgA1	arabinogalactan pr	small hypothetical	salivary protein P	hypothetical prote	MHC class I HLA-J	sepiapterin reduct	_	11 Ig	ᅮ		troponin T 2fa - r	H+-transporting AT	H+-transporting AT	extensin - tomato	mucin - sheep (fra	neural cell adhesi	hypothetical prote		gp18 protein - Myc	hypothetical prote		H+-transporting AT	gene insl protein	n cat	aspartate transcar
SUMMARIES	ID	A60726	S63324		I40692			S10782					154515					T11184		Ø				G			T11105		S019	S5117
	Length DB	54 2	~	7	25 2	9	_		7	80	7	4	_	6	۰	8	'n	S	2	0	5	0		_	~	4	S	7	7	7
æ	Query	23.5	18.7		16.9	ė.		14.7	14.7	14.6	14.4	٠		14.2					13.6	•		13.2	•	٠	•		13.2	•	13.1	12.9
	Score	7.1	56.5	ഹ	51	20	47	4	44.5	4	ω.	43.5	43	43	42	42	42	42	41	40.5	40	40	40	40	40	40	40	4	39.5	39
	Result No.	-	7	e	4	2	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote hypothetical prote kappa-casein - bov serpin I - horse ( DNA-binding proteil autoimmune epitope neural cell adhesi hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote in proteil proteil hypothetical proteil	
S17672 S23202 S23202 S24338 S24338 A37238 A37234 F176648 T36648 T36648 S62360 S24713 S72213	
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00000000000000000000000000000000000000	
38 38 38 38 38 38 38 38 37 5 5 37 5 37 5	
WWWWWWWWW444444 OHKW4WMVWWOHKW4W	

## ALIGNMENTS

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mucin, gallbladder - bovine (fragments)
C;Species: Bos primiqenius taurus (cattle)
C;Species: Bos primiqenius taurus (cattle)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C;Accession: A60726
R;Afdhal, N.H.; Offner, G.D.; Smith, B.F.
Gastroenterology 99, 1493-1501, 1990
A;Title: Characterization of bovine gallbladder mucin. Amino acid sequences of tryptials Accession: A60726
A;Accession: A60726
A;Accession: A60726
A;Accuse: preliminary
A;Molecule type: protein
A;Residues: 1-54 <AFD>
                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 STSPIRSMAPGAVHLPQPVSIRSQHT-QPIPEPSIAPSTSF---LLPMGPSPPA 51
                                                                                                                                                                                                                                                                                                                                                                         Length 54;
                                                                                                                                                                                                                                                                                                                                                                         Score 71; DB 2; Length 54;
Pred. No. 2.3;
6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                            23.5%;
35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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## RESULT

A;Cross-references: EMBL:271614; NID:g1302466; PID:e239576; PID:g1302467; GSPDB:GN000 A;Experimental source: strain S288C G;Genetics: C;Genetics: A;Gene: NIPS:YNL338w A;Gene: NI S63324
hypothetical protein YNL338w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein N0170
NyAlternate names: hypothetical protein N0170
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 05-Nov-1999
C;Accession: S63324
R;Obermaler, B.; Piravandi, E.; Rinke, M.
Submitted to the Protein Sequence Database, April 1996
A;Reference number: S63317 A; Accession: S63324 A; Molecule type: DNA A; Residues: 1-52 <OBE>

Gaps ä Length 52; 20; Indels DB 2; 18.7%; Score 56.5; D 35.7%; Pred. No. 42; iive 4; Mismatches Conservative Local Similarity les 15; Conserv Query Match Best Local Si Matches 15;

4

8 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49 11 SMOYSDIYIPTPTHTHT-PTPHPH--PHTHTHHNPNP 49 ò 셤

exp

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C;Accession: T36022
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T36022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as serum proteins. Major 'enamelin' is
C;Keywords: hydroxyproline F;6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 1 - lamb's-quarters
C;Species: Chenopodium album (lamb's-quarters)
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptomyces coelicolor
C;Date: ()3-Dec_1999 #sequence_revision ()3-Dec-1999 #text_change ()3-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG
                                                                                                                                                                                                                                                                                                                                                                                                                             small hypothetical protein SCC54.09c - Streptomyces coelicolor
                                                                                                             Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                          Score 50; DB 2; Le
Pred. No. 1.4e+02;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 2; Le:
Pred. No. 1.7e+02;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%; Score 44.5; DB 2; 28.8%; Pred. No. 5.3e+02; tive 2; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <SEE>
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R; Doerfel, P.; Weihe, A.; Dolferus, R.; Boerner, T.
                                                                                                                                                                                                                                                                               6 PPAPAPKAPAPAPVPEASTAPVAA--PTTXPSPPA 38
                                                                                                                                                                                                                           17 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: S10782
R;Strawich, E.; Glimcher, M.J.
Eur. J. Blochem. 191, 47.56, 1990
A;Title: Tooth 'enamelins' identified mainly
A;Reference number: S10780; MVID:90336641
A;Accession: S10782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                salivary protein P-B - bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: proline-rich peptide P-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 PVSTRSQHTQPTPEPSTAPSTSF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%;
                                                                                                          16.68;
37.18;
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                                                                                                             Query Match 16.6'
Best Local Similarity 37.1'
Matches 13; Conservative
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Best Local Similarity ?
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A; Residues: 1-57 <STR>
C; Superfamily: proline-r*
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Matches 15; Conserv
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14.0692
cenA protein (IgAlh) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession: 140692
R;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren FEMS Microbiol. Lett. 92, 199-204, 1992
A;Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S07073

Sarabinogalactan protein - Italian ryegrass (fragments)

C;Species: Lolium multiflorum (Italian ryegrass)

C;Species: Lolium multiflorum (Italian ryegrass)

C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998

C;Accession: S07073

R;Gleeson, P.A.; McNamara, M.; Wettenhall, R.E.H.; Stone, B.A.; Fincher, G.B.

Biochem. J. 264, 857-862, 1989

A;Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-A;Reference number: S07073; MUID:90147544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:S34439; NID:g249178; PIDN:AAB22153.1; PID:g249179
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                  of
                                                                                                     glycoprotein Ib alpha variant B - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 170082
C;Accession: 170082
C;Accession: 170082
S;Lopez, J. A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-25 < RES>
A;Residues: 1-25 < RES>
A;Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PTSEPAPSPT-TPEPTSEPAP-SPTTPEPTSEPAPS---PTTPEP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55.5; DE Fred. No. 41; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.9%; Score 51; DB Best Local Similarity 46.2%; Pred. No. 60; Matches 12; Conservative 1; Mismatches
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A; Status: preliminary
A; Molecule Type: protein
A; Residues: #46 <GLE>
A; Note: 19-Hib, and 23-Leu were also found
                                                                                                                                                                                                                                                                                                                                A; Reference number: 155355; MUID:92250564
A; Accession: 170082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 18.4%;
Local Similarity 35.6%;
les 16; Conservative
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A; Residues: 1-42 <RES>
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Best Local S
Matches 16
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A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-54 <TET>
A; Residues: 1-54 <TET>
A; Cross-references: GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF39005.1; PID:g719
A; Experimental source: strain Nigg (MoPn)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                      R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999
C;Accession: 154515
R;Bauer, T.R.; McDermid, H.E.; Budarf, M.L.; Van Keuren, M.L.; Blomberg, B.B.
Immunogenetics 38, 387-399, 1993
A;Title: Physical location of the human immunoglobulin lambda-like genes, 14.1, 16.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pre-B cell Ig lambda-like omega light chain (non-rearranging) IGLL2 - human (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A46662
collagen alpha 2(V) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1993 #sequence_revision 10-Nov-1994 #text_change 20-Jul-1995
C;Accession: A46662
                                                                                                                                                                                                                                             hypothetical protein TC0127 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: D81737
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 6.1e+02;
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Pred. No. 3.8e+02;
2; Mismatches 13;
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A;Molecule type: DNA
A;Residues: 1-31 <RES>
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A; Accession: I54515
                                                                                       20 VSTRSQHTQPTPEPSTAPSTSFLLPMGP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 QPTPEPSTAPSTSFLLPMGPSPPAEGST 55
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Best Local Similarity 42.9%;
Matches 12; Conservative
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nilarity 37.5%;
Conservative
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Best Local Similarity
Matches 9; Conserv
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C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession : 156139; 172807
R; Messer, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Welss, E.H.; Girdlestone, J.
J. Immunol. 148, 4043-4053, 1992
A; Title: HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Implic A; Reference number: 156139; MUID:92291530
A; Reference number: 156139
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date:: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Sep-1997
C;Accession: S32108
R;Maler, J.
Submitted to the EMBL Data Library, March 1993
A;Reference number: S32108
A;Reference number: S32108
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Realdues: 1-28 <RES>
A; Cross-references: GB: M80468; NID: 9188481; PIDN: AAA36306.1; PID: 9188482
A; Accession: 172807
Plant Moli Biol. 17, 155-156, 1991
A;Title: DNA sequence of a mitochondrial plasmid from Chenopodium album.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M80469; NID:g188483; PIDN:AAA36307.1; PID:g188484
C;Genetics:
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                                                                                                                                                                                                                                                                                                      Length 57;
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                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                   Score 44.5; DB 2;
Pred. No. 5.3e+02;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                            16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LPWYLRTLTFRRVP-PDPSQAPNFNHSLSLNPPSAAVG 57
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A;Molecule type: DNA
A;Residues: 1-28 <RE2>
                                                                         A;Reference number: S16587; MUID:91329724
A;Accession: S16587
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 < ADOE>
A;Cross-references: EMBL:X58911
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                                                                                                                                                                                                                                                                                                Query Match 14.7%;
Best Local Similarity 34.2%;
Matches 13; Conservative
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A;Residues: 1-47 <MAI>
A;Cross-references: EMBL:221947
C;Keywords: oxidoreductase
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Matches 9; Conservative
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S32108
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Search completed: July 13, 2001, 17:41:18
Job time: 165 sec
R;Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.
J. Biol. Chem. 268, 9381-9386, 1993
A;Title: Isolation and characterization of the chains of type V/type XI collagen present A;Accession: A46662; MUID:93252802
A;Accession: A46662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-39 <AAY>
A;Residues: 1-39 <AAY>
A;Residues: 1-39 <AAY>
A;Residues: 1-39 <AAY>
A;Residues: 1-30 <AAY
A;Resid
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C;Superfamily: troponin T
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Pred. No. 4.8e+02;
0; Mismatches 7; Indels
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Pred. No. 5.4e+02;
3; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                troponin T 2fa - rabbit (fragment)
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 41.4%;
Matches 12; Conservative
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Matches 11; Conservative
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A; Molecule type: protein
A; Residues: 1-36 < DUB>
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us-09-800-909-2\_copy\_201\_257.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 13, 2001, 17:41:23 ; Search time 9.89 Seconds (without alignments) 197.428 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-800-909-2\_COPY\_201\_257 302 1 TSTSPTRSNAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

4271 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	3820 s	P02814 homo sapien	996 gadus				P09542 mus musculu	Q9t9d5 paralichthy							P81438 myrmecia qu	rhea amer	drosoph		Q24395 drosophila		Q9xkz5 aythya amer		P43511 lymantria d		P12508 human immun		P24948 cyprinus ca		P15466 sus scrofa	P81728 rattus norv	80	9xn3	P80069 mycobacteri
SUMMARIES	OI.	N78_	PRPB_HUMAN	ATP8_GADMO	VG18_BPMD2	ATP8_PELSU	TA6P_HUMAN	MLEV_MOUSE	ATP8_PAROL	FOR2_MYRGU	RPOK_HALMA	YPU3_RHOCA	ATP8_SQUAC	CA11_RABIT	ATP8_SALAL	FOR1_MYRGU	ATP8_RHEAM	M84C_DROME	H5_COLLI	MTK_DROME	PH68_HUMAN	ATP8_AYTAM	CAPP_METEX	PBAN_LYMDI	ZNT4_BOVIN	TAT_HV1J3	ATP8_CARAU	ATP8_CYPCA	ATP8_LOXNO	RNL1_PIG	- 1	ATP8_LATCH	E	A45K_MYCBO
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021401 struthio ca P07448 rattus norv P01247 equisetum a P19755 escherichia P34105 pcrossostoma P00269 desulfovibr O18417 drosophila P17977 rattus norv P27205 ensis minor P19376 strongyloce P80264 solanum tub	S	52 AA. update) on update) 1 S'REGION.	ır's yeast). Saccharomycotina; Saccharomycetes; etaceae; Saccharomyces.	Rinke M.; EMBL/GenBank/DDBJ databases. 217C.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).	)57A1 CRC64;	DB 1; Length 52; ); is 20; Indels 3; Gaps 2; pwGPSP 49  :	AA. te) date) IDE P-A]. Vertebrata; Euteleostom1;
DETS_RAT DETS_RAT UCRQ_EQUAR YPC4_ECOLI ATPB_CROLA PEN1_BENVA RUBR_DESVH A/OA_DROSE GATG_RAT EM1_ENSMI H1S_STRPU	ALIGNMENTS	2017	9 . 2	Rinke M.; EMBL/GenBank/ R217C.	yright. It is of Bioinform Institute. Trilons as long is not remove agreement (Se isb.ch).	C1E4066D43E057A1	Score 56.5; D Pred. No. 30; 4; Mismatches PEPSTAPSTSFLLPM	PRT; 57  uence upda octation up catins: PEPT Craniata;
00.3 00.3		T 1 YEAST YN78_YEAST STANDARD; P53820; 01-0CT-1996 (Rel. 34, Created) 01-0CT-2000 (Rel. 40, Last seq 01-0CT-2000 (Rel. 40, Last ann HYPOTHERICAL 6.0 KDA PROTEIN I	cerevisiae (Ba 1gi; Ascomycota 1les; Saccharom	E FROM N.A. Pr. B., Piravandi E., ed (MAY-1996) to the LARITY: TO YEAST YHR	This SWISS-PROT entry is copyrigh between the Swiss institute of B the European Bioinformatics Institutions modified and this statement is no entities requires a license agree or send an email to license@isb-s	CAA96274.1;; CAA96273.1;2; YNL338W. protein.; AA; 5951 MW;	tch 18.7%; Score 56.5; DB 1; al Slmilarity 35.7%; Pred. No. 30; 15; Conservative 4; Mismatches 20 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP	DARD; 1, Cr 1, La 8, La 8, La E P-B Chor Prim
33.5 3.5 3.6 3.5 3.6 3.6 3.6 3.6 3.6 3.6 3.6 3.6 3.6 3.6			Saccharomyces cerevisiae Eukaryota; Fungi; Ascomy Saccharomycetales; Sacchi NCBI_TaxID=4932;	[1] SEQUENCE FROM Obermaler B., Submitted (MAY	This SWISS-PRC This SWISS-PRC between the Surpean the European use by non: modified and t entities requi	EMBL; 271614; EMBL; 271613; SGD; S0005282; Hypothetical F SEQUENCE 52	Query Match Best Local Similarity Matches 15; Conserv  8 SMAPGAVHLPQPV5  11 :::   11 :::   11 SMQYSDIYIPTFF	HUMAN PRPB_HUMAN PO2814; 21-JUL-1986 21-JUL-1999 PROLINE-RICH HOMO SADIENS BUKARYOTA; MAMMANIA; EM BUKARYOTA; MAMMANIA; EM MAMMANIA; EM
		N 1	0000 0000	RR RP CC CC	3888888888	S K D D R S S S S S S S S S S S S S S S S S	Que Bes Mat Qy Db	RESULT PRPB_H ID P AC AC DT 2 DT 2 DT 2 DT 1 DT 1 C C C C C C C C C C C C C C C C C C C

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SEQUENCE FROM N.A
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O64211;
                                                                                                                               SEQUENCE
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ID VG18_B
ID VG18_B
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DE GENE I
GN 118.
OS MYCODA
OC VITUGE
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RP SEQUE
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                                                            MEDLINE-80006513; PubMed-479131;
Isemura S., Saitoh E., Sanada K.;
"Isolation and amino acid sequences of proline-rich peptides of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-NORWEGIAN COASTAL 1;

STRAIN-NORWEGIAN COASTAL 1;

JOHANSEN 5., Bakke I.;

JOHANSEN 5., Bakke I.;

The complete mitochondrial DNA sequence of Atlantic cod (Gadus morhua): relevance to taxonomic studies among codfishes.";

Mol. Mar. Biol. Biotechnol. 5:203-214(1996).

-I- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

-I- SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-I- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=NORWEGIAN COASTAL 1; TISSUE-Liver;
MEDLINE-20174958; PUbMed-2308841;
Johansen S., Guddal P.H., Johansen T.;
"Organization of the mitochondrial genome of Atlantic cod, Gadus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROFEIN 8 (EC 3.6.1.34) (ATFASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PIRSMAPGAVHLPQPVSIRSQHTQPTPEPSIAPSISFLLPMGPSPPAEGSIG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PRGPYPPGPLAPPQPFG--PGFVPPPPPPYGPGR-----IPPPPPAPYGPG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

14.7%; Score 44.5; DB 1; Length 57;

Best Local Similarity 28.8%; Pred. No. 3.4e+02;

Matches 15; Conservative 2; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE P-A.
PYRROLIDONE CARBOXYLIC ACID.
2085FBB83BAFD063 CRC64;
                                                                                                                                                               whole saliva.",
J. Bicchem. 86:79-86(1979).
-i- PTM: P-A IS PROBABLY A DEGRADATION PRODUCT OF P-B.
PIR; A03:297; PJHUSB.
                                                                                                                                                                                                                                                                                                                                            PROLINE-RICH PEPTIDE P-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 18:411-419(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X17659; CAA35655.1; -.
EMBL; X99772; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                               5810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                            57
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                            Repeat; Saliva.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTATP8 OR ATP8
                               rissue-saliva;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP8_GADMO
P15996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                morhua."
                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP8_GADMO
ATP8_GADMO
ATP8_GADMO
ATP8_GA
DT 01-APR
DT 01-APR
DT 01-APR
DT 01-APR
DG GAGUS:
OC GACLING
OC ACCING
OC A
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-98300335; PubMed-9636706; Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.; "Genome structure of mycobacteriophage D29: implications for phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostom1;
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01-OCT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L)
InterPro; IPR001421; -. Pfam; PF00895; ATP-synt_8; 1. Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. TRANSMEM 4 24
                                                                                                                                                                                                       Score 42; DB 1; Length 55;
Pred. No. 5.3e+02;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF022214; AAC18458.1; -.
SEQUENCE 51 AA; 5680 MW; EF85B1AFF5786A34 CRC64;
                                                                                                         4 24 POTENTIAL.
55 AA; 6481 MW; E85C81E63DB48B15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pelomedusa subrufa (African side-necked turtle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1;
Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 AA
                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 RLIAAGGWKRPRKPRT----TKPKPAPKQEPAT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 RSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                      16 LPQPVSTRSQHTQPTPEPSTAPSTS 40
                                                                                                                                                                                                                                                                                                                                                                      24 LPPKVMAHTFPNEPSPQGMTTPKTA 48
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                                                                                                                                                                                                          13.9%;
32.0%;
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.29
Best Local Similarity 33.39
Matches 11; Conservative
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENE 18 PROTEIN (GP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterlophage D29.
                                                                                                                                                                                                                                     Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-28369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=44522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mucleic Acids Res. 16:10037-10052(1988).
**Incleic Acids Res. 16:10037-10052(1988).
**Incleic Acids Res. 16:10037-10052(1988).
**Incleic Acids Res. 16:10037-10037-10052(1988).
**Incleic Acids Res. 16:10037-10037-10057-10037-10057-10037-10057-10037-10057-10037-10057-10037-10057-10037-10057-10037-10057-10037-10057-10037-10037-10057-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-10037-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Promoter analysis of myosin alkali light chain genes expressed in mouse striated muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Bothidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki K., Yokoyama Y., Asahida T., Toyohara H.,
                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89057447; Pubmed-3194193;
Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 12.6%; Score 38; DB 1; Length 51; Similarity 26.3%; Pred. No. 1.1e+03; 10; Conservative 6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CE513ECBA3C8258D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PEPKKDDAKAAAPKAAPAPAAAPAAAAAPAAAPERPERPKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 POPVSTRSOHTOP -- TPEPSTAPSTSFLLPMGPSPPAE
                                                                51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin; Muscle protein; Multigene family.
1 INIT_MET 0 0
1 NON_TER 5.1 5.1
SEQUENCE 51 AA: 5085 MW; CE513ECBA3C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X12972; CAA31415.1; -. PIR; S01945; S01945.
HSSP; P04002; lATF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C3H; TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                STANDARD;
                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buckingham M.E.
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                                                                                                                                                                                                                                                                                  MYL3 OR MLC1V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saitoh K., Ha
Yamashita Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP8_PAROL Q9T9D5;
                                                                MLEV_MOUSE
                                                                                                                                                                                                                                                        (FRAGMENT)
                                                                                             P09542
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP8_PAROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                      FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX. SUBCELLULAR LOCATION: MEMBRANE-BOUND. SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"A 56 aa polypeptide with phosphorylation motif, potentially associated with Tap2 isoform activity.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAY BE ASSOCIATED WITH TAP2 ISOFORM ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00895; ATP-synt_8; 1.
Hydrogen 1on transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 4 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 55;
Pred. No. 7.8e+02;
3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 39; DB 1; Length 56; 40.0%; Pred. No. 9.6e+02; 1ve 4; Mismatches 8; Indels
                             (DEC-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AA; 6536 MW; D8D4BC8F8651A001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
TAP2-ASSOCIATED 6.5 KDA POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%; ; 36.0%; I
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Best Local Similarity 36.0v
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Matches 8; Conserv
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Q9Y3F1;
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Length 51;

57 AA

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Haloarcula marismortui (Halobacterium marismortui).
Archaea: Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
NCBI_TaxID=2238;
                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
3 PNPVNTK-----PTPYP 14
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR: E41715; E41715.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                           RPOK_HALMA
P29200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
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P26159;
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                                                                                                 RPOK_HALMA
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@1sb-sib.ch).
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                                                                                                 -i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHOMPIAL ATPASE COMPLEX.
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-i- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myrmecia gulosa (Red bulldog ant).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Formicoidea; Formicidae; Myrmecia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98165787; PubMed=9497332;
MACKINCE=98165787; PubMed=9497332;
MACKINCS J. S., Veal D.A., Beattie A.J., Gooley A.A.;
MACKINCON J.S., Veal D.A., Beattie A.J., Gooley A.A.;
Isolation from an ant Warmecia gulosa of two inducible
O-glycosylated proline-rich antibacterial peptides.";
J. Blol. Chem. 273:5139-6143(1998).
-i- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
     "The complete nucleotide sequence of Japanese flounder mitochondrial
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PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE,
GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
SIMILARITY: TO DROSOPHILA DROSOCIN.
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InterPro; IPR001421; -.
InterPro; IPR00314; -.
Pfam, PF00695; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SEQUENCE 55 AA; 6571 MW; 2B5EFE20FDCB6AA9 CRC64;
                              genome: structural property and cue for resolving teleostean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 37.5; DB 1; Length 16; 47.1%; Pred. No. 3.9e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 38; DB 1; Length 55; 29.2%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
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16 AA; 1807 MW; 9C3CA3B00BC2EGAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Best Local Similarity 29.2.
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                                                     relationship."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 176:4754-4756(1994).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94321350; PubMed-8045907;
McKuue K., Woychik N.A.;
"Halobacterial S9 operon contains two genes encoding proteins
homologous to subunits shared by eukaryotic RNA polymerases I, II,
                                                                                                                                                                                                                                                      ø
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MEDLINE-92105119; PubMed-1840597; Kroemer W.J., Arndt E.; Rroemer W.J., Arndt E.; Pardt E.; Pard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
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Pfam; PF01192; RNA_pol_K; 1.
PROSITE; PS01111; RNA_POL_K_14KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription.
Transferase; SNA-directed RNA polymerase; Transcription.
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42.9%; Pred. No. 1.3e+03;
tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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01-OCT-2000
01-OCT-2000
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Arch. Bioc
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MOD_RES
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SEQUENCE
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ATP8_SALAL
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                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasmussen A.S., Arnason U.; Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes."; J. Mol. Evol. 48:118-123(1999).
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBMIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
                       Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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M
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001421; -. Pfam; PF00895; ATP-synt_8; 1. Hydrogen lon transport; CF(0); Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                       Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
HYPOTHETICAL 5.8 KDA PROTEIN IN PUHA 5'REGION (ORF55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photosynthesis; Hypothetical protein.
SEQUENCE 55 AA; 5750 MW; 7EB55296266D48B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 POTENTIAL.
6587 MW; 3FB9F843CEFA54EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.5; DB 1;
Pred. No. 1.5e+03;
2; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 QPVSTRSQHTQPTPEPS--TAPSTSFLLPMGPSP-PA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 RPNSAAPARRQPWPCGSCVTAPVAVRIGAMGASPGPA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squalus acanthias (Spiny dogfish). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99091711; PubMed-9873084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.1%;
Best Local Similarity 40.5%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z11165; CAA77517.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S17805; S17805
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                                                                                                                                    SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=1061;
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Q9ZZ50;
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ATPB_SQUAC
ID ATPB_SQUAC
ID 30-MAY
DT 30-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONVERTED TO AN ALDEHYDE GROUP THAT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arch. Blochem. Blophys. 138:443-450(1970).
-!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
-!- FUNCTILLAR FORMING COLLAGEN).
-!- SUBUNIT: TRIMERS OF ONE ALPHA 2(1) AND TWO ALPHA 1(1) CHAINS.
-!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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80
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Bornstein P., Nesse R.;
"The comparative blochemistry of collagen: the structure of restin comparative blochemistry of collagen: the structure of restin collagen and its relevance to immunochemical studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 1; Length 53; Pred. No. 2e+03;
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HYDROXIATION (PROBABLE).
HYDROXILATION (PROBABLE).
HYDROXILATION (PROBABLE).
HYDROXILATION (PROBABLE).
HYDROXILATION (PROBABLE).
HYDROXILATION (PROBABLE).
Length 55;
                                            12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG
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                 . 1.7e+03;
Score 36; DB 1;
Pred. No. 1.7e+03
                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                53 AA
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                                              2; Mismatches
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                                                                                             ----PEPSTAPST 39
                                                                                                                                       22 VILPKKVMTHLFNNNPTAKSAEKPKPEPWNWPWT
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                                                                                                                                                                                                                                                                PRT;
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11.9%;
35.3%;
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30.2%;
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4987 MW;
                                                                                           14 VHLPQPVSTRSQHTQPT----
            Best Local Similario,
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                                                                                                                                                                                             SEQUENCE FROM N.A.

Doiron S., Blier P.U., Bernatchez L.;

"A comparative analysis of complete sequence of mitochondrial genome between brook char (Salvelinus fontinalis) and arctic char (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PINDCTION: UPON BACTERIAL CHALLENGE.
-i- PIM: O-LINKED GIYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
-i- SIMILARITY: TO DROSOPHILA DROSOCIN.
Antibiotic: Glycoprotein; Insect immunity; Hemolymph.
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus. NCBI_TaxID=8036;
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SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
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Pram: PF00855; APF-Synt_8; 1.

Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. SEODENCE 55 AA: 6455 MW; 71E430C2E346924A CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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ATP SYNTHASE PROTEIN 8 (EC 3.6.1. MATATP 0 Rx ATPB OR ATPASE8. Salvelinus alpinus (Arctic char). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF154851; AAD41389.1; -.
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FOR1_MYRGU
ID FOR1_MYRGU
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FT CARBOHYD 11 11 0-LINKED (GALNAC. ..).

SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2EOAE CRC64;

Query Match

Best Local Similarity 41.2%; Pred. No. 7e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 5; Gaps

QY 17 POPVSTRSQHTOPTPEP 33

QY 17 POPVSTRSQHTOPTPEP 33

QY 17 POPVSTRSQHTOPTPEP 14

Db 3 POPVNNK----PTPHP 14
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Search completed: July 13, 2001, 17:44:04 Job time: 161 sec 092300 human respi 092311 human respi 042311 human respi 079966 mogurnda ad 079968 mogurnda ad 041179 chlamydomon 041179 chlamydomon 091fe6 vaccinia vi 092309 human respi 092310 human respi 092310 human respi 092319 human respi 092319 human respi 051319 human respi 051317 human respi 051317 human respi 051317 human respi 051318 human respi 051318 human respi 051318 human respi 091408 artus norv 091421 human respi 091311 human respi 091311 human respi 091311 human respi 091311 human respi

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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Ishida F.; Submitted (JUL-1995) Submitted (JUL-1995) ERBL; 139103; AAA6949 InterPro; IPR02465; PRINTS; PR01217; PRIC NON_TER 1 S2 SEQUENCE 52 AA; 51 CY MAtch L Local Similarity ches 17; Conservat	PRÉL   1   1   1   1   1   1   1   1   1   1
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STRAIN=181691;
Cogqins W.B., Lefkowitz E.J., Sullender W.M.;
Cogins W.B., Lefkowitz E.J., Sullender W.M.;
Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086872; AAC42992.1;
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InterPro; IPR000925; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-203721;
Cogqins W.B., Lefkowitz E.J., Sullender W.M.;
Cogins W.B., Lefkowitz E.J., Sullender W.M.;
Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AnG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARG6888; AAC43008.1;
InterPro: IPR000925;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Pred. No. 82;
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Pred. No. 82;
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Paramyxoviridae; Pneumovirinae; Pneumovirus
NCBI_TaxID=11250;
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(FRAGMENT).
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Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Cre
01-JUL-1997 (TrEMBLrel. 04, Las
01-JUN-2000.TrEMBLrel. 14, Las
HUNTINGTIN PROTEIN (FRAGMENT).
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31.8%;
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5613 MW;
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Matches 14; Conservative
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Matches 12; Conserv
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NCBI_TaxID=11250;
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SEQUENCE
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                                                                                                                                                                                  Lopez J.A., Ludwig E.H., McCarthy B.J.;

"Polymorphism of human glycoprotein Ib alpha results from a variable number of tandem repeats of a 13-amino acid sequence in the mucin-like macroglycopeptide region. Structure/function implications.";
J. Blol. Chem. 267:10055-10051(1992).

EMBL; S34439; AAB22153.1;
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"Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086886; AAC43006.1; -
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                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                               42 AA; 4222 MW; 228018AC7FBE3F38 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-2000 (TrEMBLrel. 15, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
Human respiratory syncytial virus.
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NCBI_TaxID=11250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 HTSOKETLHSTSSEGNPSPSQVYTTSEYLSQSPSP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55.5; |
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human respiratory syncytial virus.
                                                                                                                                                              MEDLINE-92250564; PubMed-1577776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000925; -. Pfam; PF00802; Glycoprotein_G; 1.
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5541 MW;
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ilarity 34.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%;
ilarity 35.6%;
Conservative
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Best Local Similarity
Matches 16; Conserv
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52 AA;
                                                                                                                             SEQUENCE FROM N.A.
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                                                                                NCBI_TaxID=9606;
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Best Local Simi
Matches 12;
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46 AA; 4592 MW; FCE1D38D8DEDC173 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10633;
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SEQUENCE
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09J7C8;
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Q9J7C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                               SEQUENCE FROM N.A.
MEDLINE-96326790; PubMed-8766138;
Percheux C., Gall A.L.; Kaplan J.C., Dode C.;
Sequence analysis of the CAG triplet repeats region in the Huntington disease gene (IT15) in several mammalian species.";
Ann. Genet. 39:81-86(1996).
EMBL; S83377; AAB50771.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Teichert A.M., Karantzoulis-Fegaras F., Wang Y., Mawji I.A., Bei X., Gnanapandithen K., Marsden P.A.;
"Characterization of the murine endothelial nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                Length 33;
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                                                                                                                                                                                                                                                                                            33 AA; 3393 MW; 44F558CE5636722A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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llarity 47.8%; Pred. No. 96;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 50.5; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter.";
Blochim. Blophys. Acta 1443:352-357(1998).
EMBL; AF091262; AAD22613.1; -
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01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-NOV-1999 (TrEMBLrel. 12, Last anno
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                                                                                                                                                                                                                                                                                                                                                                             16.78;
38.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 15; Conserv
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NCBI_TaxID-9595;
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Q9GL38;
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Chung H.Y., Davis M.E., Hines H.C.;
"PCR-SSCP analysis of the bovine calpastatin gene domain L region.";
"PCR-SCP analysis of the bovine calpastatin gene domain L region.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY008267; AAG23869.1; -.
NON_TER 1 1
NON_TER 52 52
SEQUENCE 52 AA; 5749 MW; CBD5A7449AFDDA89 CRC64;
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Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
"Clones from the human gene complex coding for salivary proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 SMAPGAVHLPQP-VSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 55
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                                                                                                                                                                                                                                                                               Indels
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
LARGE ANTIGEN (FRAGMENT).
Simian virus 40 (SV40).
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                               19:
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EMBL; K02578; AAA36505.1; -.
                                                                                                                                                                                                                              Score 50; DB 6;
Pred. No. 1e+02;
3; Mismatches 1
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                                                                                                                                                                                                                                16.6%;
33.3%;
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Best Local Similarity 33.39
Matches 11, Conservative
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InterPro; IPR000925; -.
Pfam; PF00802; Glycoprotein_G; 1.
NON_TER 1 1
SCOUENCE 5.2 SS
SEQUENCE 5.2 AA; 5530 MW; C202
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NON_TER
SEQUENCE
                                                                                                                                                                   Query Match
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Q9HB17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     мопака М., Nonaka М., Takenaka О., Okada N., Okada Н.;
"A new repetitive sequence uniquely present in the decay-accelerating
factor genes.";
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-182473;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
"Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AUG.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF086873; AAC42993.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
                                                                                                  4
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                                            Score 49; DB 4; Length 46;
Pred. No. 1.2e+02;
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                                                                                             15; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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                                                                                             2; Mismatches
                                                                                                                                          21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS 54
                                                                                                                                                                                      1 SARS----PPRKPQGPPQQEGNNPQGPPPAGGN 30
                                                                                                                                                                                                                                                                                                    51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenetics 47:246-255(1998).
                                                 16.2%;
38.2%;
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1 Similarity 28.9%;
13; Conservative (
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5545 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB003315; BAA22903.1;
Complement pathway.
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ATTACHMENT GLYCOPROTEIN G (F
                                                                                             13; Conservative
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                                              Query Match
Best Local Similarity
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Best Local Similarity
Matches 13; Conserv
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SEQUENCE FROM N.A.
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AC 018723
DT 01-NOV
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Cogglas W.B., Lefkowitz E.J., Sullender W.M.;
Cogglas W.B., Lefkowitz E.J., Sullender W.M.;
Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (ANG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF086874; AAC42994.1;
InterPro; IPR000925;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           Length 52;
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                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA nėgativė-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pirone D.M., Fukihara S., Gutkind S.J., Burbelo P.D., "SPECS, small binding proteins for CDC42 proteins."; J. Biol., Chem. 0.0-01.2000)
EMBL, AF286592; AAG17723.1; -...
                                                                                                                                                                            6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
                                                                                                                                                                                                         6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
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C2029E4C5B551270 CRC64;
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4245 MW; 3B416F3C5ADF4E91 CRC64;

    Last sequence update)
    Last annotation update)
    (FRAGMENT)

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 49; DB 14;
31.8%; Pred. No. 1.3e+02;
tive 4; Mismatches 26,
                                                                           Score 49; DB 14;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                            52 AA
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                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human respiratory syncytial virus.
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                                                                           16.2%;
31.8%;
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                                                                                                                             Conservative
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                                                                                                      Best Local Similarity
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Matches 14; Conserv
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                                                                                                Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last squence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
MYDKI.
Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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"Integration of porcine chromosome 13 maps.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF222917; AAG41130.1; -.
Query Mtch 15.9%; Score 48; DB 4; Length 38; Best Local Similarity 46.7%; Pred. No. 1.3e+02; Matches 14; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 48; DB 6; Length 42; 36.6%; Pred. No. 1.4e+02; tive 2; Mismatches 14; Indels
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42 42
42 AA; 4677 MW; 78BDD867E66EF64F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 AA.
                                                                                                                                                                   14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLL 43
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Best Local Similarity 36.6'
Matches 15; Conservative
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SEQUENCE
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AC 096KJ3
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AC 096KJ3
AC 01-MAR
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Search completed: July 13, 2001, 17:43:47 Job time: 164 sec

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July 13, 2001, 17:38:03 ; Search time 19.91 Seconds (without alignments) 173.559 Million cell updates/sec
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1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57
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/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                 US-09-800-909-2_COPY_201_257
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_0601:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l length: 0
| length: 57
                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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Maximum I
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                                                                                                                                                                                                                                                                 Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

	Description	Human secreted pro	Amino acid sequenc	Linking B region #	Sequence of a pept	Camel Iq 2-heavy c	Peptide encoded by	Amphotropic hyperv	Human INTERCEPT 21	Human ORFX ORF2454	Sequence of human	Human 5' EST relat
•	·	AAB56300	AAW59911	AAR15261	AAR49722	AAR49536	AAY01285	AAW88522	AAB61193	AAB42690	AAP81606	AAY65289
	DB	21	19	12	15	15	20	20	22	21	6	
	Query Match Length DB ID	47	49	45	54	54	41	46	25	55	21	36
æ (		22.7	22.4	19.5	19.2	19.2	18.7	18.2	18.2	18.0	17.9	17.9
	Score	68.5	67.5	59	28	58	56.5	55	55	54.5	54	54
;	Result No.	-	7	m	4	Ŋ	9	7	89	6	10	11

H. insolens family heavy chain hinge Mucin peptide MUCI MUCIN peptide MUCI Peptide targetted Amino acid sequenc 1gA protease specification in the Human 1gAl CH2 regituman 1gAl CH2 regituman 1gAl CH2 regituman accreted man	Mucin repeat seque Human mucin peptid Linking B region # Sequence of portio Sequence of hinge Camel 2-chain ig h Carcinoma-associat Peptide encoded by Fragment of human Lck binding active Arabidopsis thalia Human Secreted pro Human Secreted pro Human Sequence of struct Gastro-interinal	Ŋ	·	1 by gene 99 SEQ ID NO:394.	Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; cardirherative; cardiant; vasotropic; cardirherative; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; pathological condition; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; autoimmune disease; racidavascular disorder; cardiac arrest; cerebral isordemia; cerebrovascular disorder; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; food additive; preservative.			PE, Komatsoulis GA, Birse CE;
AAW31691 AAW31692 AAW31697 AAW31697 AAK88860 AAX49096 AAX49681 AAW96613 AAW64623 AAW64623 AAW6463	AANGUSAS AAM72703 AAM72703 AAM15255 AAR19529 AAR49529 AAR49529 AAR48723 AAR38081 AAY38081 AAG00350 AAG00350 AAG00350 AAG00350 AAM74023	AAW 4094 AAY 961006 AAP 90040 AAP 91846 AAW 69459 AAW 69459	47 AA.	pepcoue eou	tive; cytos tive; cytos inercoprot gene thera id attrititi order; card giogenesis; on; ocular			Young DR;
118 118 118 118 118 118 118 118 118		100 100	Protein;	ry) sequence	ifera ifera interational; umato ir dis ir; an ifecti		2788.	O68. INC Ore Sope
222222222222222222222222222222222222222	04440004440400044 00170004404000044			irst entry protein se	tiprol tiprol ; noot lmolog e; rhe ascula isorde se; in		000WO-US12788	S-0. ME 8 KA
77777			standard;	1 (fire	tic; an tic; an tective ophtha dopetha cardiov cular d s disea	ens. 42-A1.		9; 99 MAN GEN Ruben Florenc
523 523 522 500 500 500 500 500 500 500 500 500	444 0000 4444 0000 4444 000000000000000	4 4 4 4 4 0.0000000	1 AB56300 AB56300;	13-MAR-2001 Human secre	uman; sec ntirheuma erebropro ingicide; itoimmune eoplasm; erebrovas lzheimer'	Homo sapie WO20007004	3-NOV-2000 1-MAY-2000	13-MAY-199 (HUMA-) HU Rosen CA, Duan RD,
73 2 2 2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	, , , , , , , , , , , , , , , , , , ,	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	356 356		KW KW ANI		1	

of plague and bacteria on teeth

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                                                                                                    The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins given in AAB56077 to AAB56362. Human secreted proteins given in AAB56077 to AAB56362. Human secreted correspond activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; cardiant; can tiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; correspond corrective; antibacterial; corrected polynucleotides and proteins can be used to prevent, treat or ameliorate polynucleotides and proteins can be used to prevent, treat or ameliorate corrected condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular carbinates e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular condisorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to requence telessues and in chemotaxis. The proteins can also be used as a condition of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

    used for prevention and removal

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.7%; Score 68.5; DB 21; Length 47; 40.5%; Pred. No. 2.4; Live 3; Mismatches 17; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 PVSTRSQHTQPTPE----PSTAPSTSFLLPMGPSPPAEGST 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of the mutanase enzyme PT box.
                                                                                Disclosure; Page 1035; 1065pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene encoding a mutanase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW59911 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0284362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96JP-0314057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 40.5 ses 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPF; 1998-474495/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIOY ) LION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteria; teeth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutanase
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Matches
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                                       This is the amino acid sequence of the mutanase enzyme PT box, which decomposes the alpha-1,3 glucoside bond of mutan. The mutanase enzyme is used in the method of the invention for prevention and removal of plaque and bacteria on teeth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fungal (hemi)cellulose degrading enzymes - for prodn. of lig. fuel gas and feed protein, have specified carbohydrate binding domain
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linking B region #8 derived from a (hemi)cellulose-degrading enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is one of B specified linking B regions which are derived from a cellulose- or hemicellulose-degrading enzyme and which are enriched in the amino acids Gly and/or Asn and/or Pro and/or Ser and/or Thr and/or Gln. It can be incorporated in a fusion protein comprising a catalytic domain from a cellulase, e.g. a Bacillus endoglucanase, and a carbohydrate binding domain from a fungal endoglucanase. See also AAR15254-R15260.
                                                                                                                                                                                                                                                                    5;
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7
                                                                                                                                                                                                                        Length 49;
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                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                1 TST-SPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP
                                                                                                                                                                                                                                                                                                                                                          2 avgipss-stsspvngptststtsttstppvgpttps-gctae 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD
                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminal A region.
                                                                                                                                                                                                                     Score 67.5; DB
Pred. No. 3.1;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 46; 73pp; English.
Claim 2; Page 5; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate;
cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR15261 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%;
                                                                                                                                                                                                                        Query Match 22.4%;
Best Local Similarity 35.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90DK-0001158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBD; hemicellulosic
Trichoderma reesei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-353766/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                         49 AA;
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Camelus dromadarius.
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                                                                                                                                                  21-AUG-1992;
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                                                                                                                                                                                                                      Casterman C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09903978-A1
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                                                                                                          EP584421-A.
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                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Region
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                                                                            Sequence of a peptide which is part of the heavy (H) chain (CH3) of an
                                                                                                                                                                                                                                                                                                                                                        A novel immunoglobulin (Ig) is claimed which comprises two heavy (H) polypeptide chains sufficient for the formation of a complete antique binding site or several such chains. The Ig is devoid of light (L) polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E. coli, by: cloning a DNA or cDNA sequence coding for the WI domain of an Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids; recovering the cloned fragment after amplification using a 5' primer contg. an Xho site and a 3' primer contg. the Spe site having the sequence in AAQ44383; cloning the recovered fragment is a vector; transforming host cells; and recovering the expression product of the VHH coding sequence. A nucleotide encoding the peptides in AAR49721-24 is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; Ig; heavy chain; constant region; variable region; antibody engineering; IgG2; IgG3.
                                                                                                                                                                                                                                                                                                           Immunoglobulins devoid of light chains - also processes for their preparation, and protein and nucleotide sequence encoding them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camel Ig 2-heavy chain molecule (clone no. 72/79).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ipgpgpkpgpgpgpgpkpgpkpepectcpkcpapellg 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58;
Pred. No.
                                                                                                         Immunoglobulin; heavy chain; Camelid
                   AAR49722 standard; peptide; 54 AA.
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                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 65; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%;
31.6%;
                                                                                                                                                                                       93WO-EP02214.
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                                                                                                                                                                                                           92EP-0402326
93EP-0401310
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                                                         (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                                                                                      Casterman C, Hamers R;
                                                                                       immunoglobulin (Iq).
                                                                                                                                                                                                                                        (CAST/) CASTERMAN C. (HAME/) HAMERS R.
                                                                                                                              Camelus dromedarius
                                                                                                                                                                                                                                                                                       WPI; 1994-083195/10
                                                                                                                                                                                      18-AUG-1993;
                                                                                                                                                                                                          21-AUG-1992:
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                                                         22-AUG-1994
                                                                                                                                                WO9404678-A.
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                                                                                                                                                                    03-MAR-1994
                                     AAR49722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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         AAR49722
RESULT
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Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein; RPRP; arabino-galactan protein; AGP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This 2-chain Ig molecule lacks any light chains. The Ig has e.g. improved solubility and aggregate much less than heavy chains of 4-chain. Igs. The Igs can be used normally for e.g. diagnosis, therapy, in vaccines, for isolation and purification of antigens and in the production of anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated immunoglobulin molecules devoid of light polypeptide chains - consisting of heavy polypeptide chains only, obtd. from Camelid serum, for use as antibodies
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                                                                                                                           41..54 /note= "heavy chain constant region"
                                                                                              "heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide encoded by HRGP gene cassette.
                                            /note- "hinge region"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 19; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY01285 standard; Protein; 41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycopeptide; internal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.2%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                         92EP-0402326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US15083.
                                                                                                                                                                                                                                                                                                         92EP-0402326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-067061/09.
                                                                                                                                                                                                                                                                                                                                                                                                           CASTERMAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 AA;
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Gaps

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17; Indels

DB 20; Length 46; 50;

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The present sequence is given in a specification relating to isolated human proteins designated INTERCEPT 217, INVERCEPT 297, TANGO 292, TANGO 312, TANGO 313. These proteins are useful as modulating agents or as targeting agents for developing agents to regulate cellular processes e.g. growth, proliferation, survival, differentiation and activity of human tissues. Discasses which can be diagnosed, prevented and treated by administration of these polypeptides, their nucleic acids and modulators include cancers, inflammatory clasmosed, prevented and isorders e.g. arrhythmia, and skin disorders e.g. profits and accoding the isolated proteins can be used to express the proteins in a host cell in gene therapy applications.

Antisense molecules or ribozymes can be used to inhibit expression of the proteins in target cells. Fragments of the nucleic acid molecules encoding the isolated proteins as the protein and as encoding the isolated proteins as the protein and as hybridisation probes and as polymerase chain reaction (PCR) primers.
hypervariable polyprolline (HP) region modified to include a heterologous protein or peptide. Retroviral vectors made targetable by modification of the HP region enable the delivery of desired genes to a variety of cell types. Unlike prior art modifications in the receptor binding region, the particle does not disrupt envelope structure to impair folding, processing, and incorporation of the envelope protein. The present sequence represents an amphotropic hypervariable polyproline region truncated peptide from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human proteins are used for diagnosis, treatment and prevention of cancers, inflammatory disorders, cardiac disorders e.g. arrhythmia, and skin disorders e.g. psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; INTERCEPT 217; INTERCEPT 297; TANGO 276; TANGO 292; TANGO 322;
TANGO 331; TANGO 332; cytostatic; antiinflammatory; antiarrhythmic;
antipsoriatic; gene therapy; cancer; inflammatory disorder;
cardiac disorder; arrhythmia; skin disorder; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                         14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                 11 vpapqpps--plntsyppsttstpstsptspsvpqpp 45
                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human INTERCEPT 217 cytoplasmic domain.
                                                                                                                                                                                                                                                                                   Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 297; 372pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB61193 standard; Protein; 52
                                                                                                                                                                                                                                                                                   18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0342364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-2000; 2000WO-US16658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kirst SJ, Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-061966/07.
                                                                                                                                                                                                                 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200100638-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB61193;
                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB61193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
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                                                                                                                                                                                                                                                                                                                       The invention relates to novel synthetic genes for plant gums. A new approach is described to the production of hydroxyproline-rich alpyroproteins (RRPRS). repetitive proline-rich proteins (RRPRS) and arabino-galactan proteins (ARPS). Synthetic genes comprising a nucleic acid encoding the peptide (AAY01267) can be engineered for the production of repetitive glycopeptide modules in cells. The invention provided a new approach to the problem of producing plant gums that is not dependent on environmental factors and greatly simplifies the production of a variety of naturally occurring gums as well as designer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                   -
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphotropic hypervariable polyproline region truncated peptide N-14.
                                                                                                                                                                                                          Novel synthetic gene designed from repetitive peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypervariable polyproline region; amphotropic .gp70 protein; human cytomegalovirus; hCMV; retrovirus; envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%; Score 56.5; 43.3%; Pred. No. 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strasppppsppppsppps---ppppspp 30
                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 72pp; English.
                                                                                                                                                                                                                                      hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUTHERN CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW88522 standard; peptide; 46
    21-JUL-1997; 97US-0897556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0856074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus
                                                                                                                                         WPI; 1999-132225/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-059696/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                 (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AA;
                                                                                                                                                                    N-PSDB; AAX27690
                                                                                               Kielszewski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9851700-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1998
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Sequence

Query Match

Best Local Matches

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AAW88522;

Barnes TS;

The present invention describes a retroviral vector particle (RVP1), having a modified retroviral envelope polypeptide which includes the

New retroviral vector particle - has envelope polypeptide modified in the hypervariable polyproline region to enable cell targeting

Disclosure; Fig 2; 79pp; English.

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AAP81606
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                                                                          ä
                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressave; antiinflammatory; antinviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidianatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage damage; antiinflammatory disease; coagulation;
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
                                                                                                                                                                                                                                                                                                                                                                                                                           allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                          .;
6
                                                  Length 52;
                                                                         Indels
                                                                                                                                                                                                                                                            Human ORFX ORF2454 polypeptide sequence SEQ ID NO:4908.
                                                                         18;
                                                                                                              DB 22;
                                                                                               19 PVSTRSQHTQPTP -- EPSTAPSTSFLLPMGPSPPAEGST 55
                                                                        5; Mismatches
                                               18.2%; Score 55; 35.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 4083; 5507pp; English.
                                                                                                                                                                                    AAB42690 standard; Protein; 55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive.
                                                           Local Similarity 35.9
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
           52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC76899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     damage;
                                                                                                                                                                                                                                    08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-0CT-2000
           Sequence
                                                                                                                                                                                                            AAB42690;
                                                  Query Match
                                                             Best Loca
Matches
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                                                                                                                                                                       AAB42690
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the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinfiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Cu/Zn superoxide dismutase (SOD) polymer of SOD units of at least 2 SOD monomers covalently coupled, carboxy terminus to amino terminus, to each other by a polypeptide spacer of at least 3 amino acids is claimed. The polymers are of formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Cu/Zn superoxidedismutase polymer; pSODCFISODHA1; human immunoglobulin A1; hinge region; antiinflammatory agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superoxidedismutase polymers having extended in vivo life comprising superoxidedismutase monomers covalently coupled polypeptide spacers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SOD monomer - IgA - SOD monomer)x or
(SOD monomer - IgA - SOD monomer - IgA - SOD monomer)x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 psgrtpsrtpptpypcphgdrllppsrp--lpagpasafppaersrg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 PVSTRSQHTQPTPEPS-----TAPSTSFLLPMGPS---PPAEGSTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of human immunoglobulin Al (IgAl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.0%; Score 54.5; D
38.3%; Pred. No. 67;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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4..20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="IgA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88EP-0302244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87US-0026143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 38.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1988-265657/38.
P-PSDB; AAN80435.
                                                                                                                                                                                                                                                                                                                                                                                                                   55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP81606;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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19A = a \cdot 10-100 amino acid long segment of an immunoglobulin hinge region \kappa = 2-4
                                         AAN80435 was used to make pSODCFISODHAI encoding bacterial expression spacer-linked human SOD monomers. AAN80435 encodes human 1gAl hinge region beginning at AA residue 226 to avoid the Cys 225 residue with BamHI and NcoI sites at its ends. The SOD polymers have an extended circulatory life and retain the activity of SOD. The cloning and sequencing of human SOD (hSOD) cDNA and prodn. of hSOD in bacteria and yeast are described in EP-138111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, 5' EST; expressed sequence taq; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel secreted protein 5' expressed sequence tag sequences used
                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5' EST related polypeptide SEQ ID NO:1450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                       .
6
                                                                                                                                                                                                                                      DB
29;
                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                       Score 54;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 788; 837pp; English.
                                                                                                                                                                                                                                                                                                        16 LPQPVSTRSQHTQPTPEPSTAPSTS 40
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY65289 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                          1 lagpvps----tpptpspstpptps 21
                                                                                                                                                                                                                                    17.9%;
48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation; identification
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-038446/03
                                                                                                                                                                                   21 AA;
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ID AAY6
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used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This peptide comprises a Humicola insolens family 45 cellulase glycosylated linker used in a novel hybrid enzyme between the cellulose binding domain (CBD) of Mycellophthora thermophila cellulase and Humicola lanuqinosa lipase (Lipolase). DNA expressing the linker was obtained by PCR (see AAT90506-07). A DNA construct encoding CBD-glycosylated linker-Lipolase is given in AAT7070. A claimed process for desizing cellulose-containing fabric or textile involves treating the fabric or textile with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic enzyme linked to a CBD. The process gives improved enzyme performance by modifying the enzyme so as to increase its affinity for cellulosic
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desizing cellulose-containing fabric or textile using an enzyme hybrid - which comprises a catalytically active amino acid sequence of a non-cellulolytic enzyme linked to an amino acid sequence
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Myceliophthora thermophila; cellulose binding domain; lipase;
Lipolase; Humicola insolens; linker.
                                                                                                                                                                                       Score 54; DB 21; Length 36;
Pred. No. 49;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Von Der Osten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. insolens family 45 cellulase linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising a cellulose binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 43; 72pp; English.
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                                                                                                                                                                                                                                                              29 PTPEPSTAPSTSFLLPMGP--SPP 50
                                                                                                                                                                                                                                                                                    AAW26641 standard; Peptide; 37
                                                                                                                                                                                            17.9%;
50.0%;
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                                                                                                                                                                                            Query Match 17.9
Best Local Similarity 50.0
Matches 12; Conservative
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                                                                                                                                            36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAW26641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                              Seguence
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20-MAR-1997;
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                                                                                                                            25-SEP-1997
                                                                                                                                                                                                                                                                                    haemocyanin
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                                                                          Synthetic.
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                                                                                      Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the heavy chain hinge region of human IgAl. IgA is secreted by adults at high concentrations in their secretions. However newborn children have no mucosal IgA of their own. Human milk is very rich in IgA providing the infant with passive immunity by coating the mucous membranes with the antibody. Some bacteria secrete IgA proteases which inactivate the infants IgA, when it starts producing it, by cleavage at the hinge region, leading to infection of the infant. The most common allotype of IgA2 has the hinge region deleted and is therefore resistant to degradation by bacterial proteases. See also AAR37993.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                             Heavy chain; hinge region; human; IgAl; IgA; secretion; adult; IgA2; newborn; children; milk; infant; passive; immunity; mucous membrane; antibody; bacteria; IgA protease; allotype; resistant.
                                                                                                                                                                                                                                                                                                                                                                                                         Infant formula contg. an IgA protease inhibitor – for providing protection against IgA protease-producing pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                      1;
  Length 37;
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                       Indels
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                     16;
  DB 18;
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Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                         51
                                                             1 vgipss-stsspvngptststststtssppvgpttps 37
                                        14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA
                     7; Mismatches
 Score 53.5; 1
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 pvs----tpptpspstppt-----psp 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
                                                                                                                                                                                                                                                                                                                                              (NEWE-) NEW ENGLAND MED CENT HOSPITALS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 25pp; English.
                                                                                                              AAR37992 standard; peptide; 21 AA
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                                                                                                                                                                            Heavy chain hinge region of IgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW35739 standard; peptide; 50
 17.78;
36.88;
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                                                                                                                                                                                                                                                                                                                          91US-0802338
                                                                                                                                                        (first entry)
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA;
                                                                                                                                                       13-OCT-1993
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                     03-DEC-1992;
                                                                                                                                                                                                                                                                                                                          04-DEC-1991;
                     14;
                                                                                                                                                                                                                                                            WO9310818-A
                                                                                                                                                                                                                                                                                 10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                   Plaut AG;
Query Match
Best Local
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                     Matches
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This mucin peptide is used in a vaccine capable of producing an immune response which recognises a mucin. The mucin peptide is selected from MUCI peptide group. The vaccine comprises an amount of the mucin peptide conjugated to an immunogenic protein effective to stimulate or enhance immune response in the subject, together with an adjuvant and a vehicle. The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its derivative. The vaccine can be used to induce an immune response in patients suffering from a cancer of the type where the cancer cells have mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine effective against cancer of the breast, prostate, colon, lung or pancreas - comprising mucin peptide, especially MUC1, conjugated to immunogenic protein, especially keyhole limpet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TSTSPIRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ppahgvt 42
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                                                              keyhole limpet haemocyanin; KHL; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 18;
Pred. No. 1.1e+02;
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                                                                                                immunogenic protein; immune response
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36.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Livingston PO, Zhang
Mucin peptide MUC1-5
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response which recognises a mucin. The mucin peptide is selected from MUCl peptide group. The vaccine comprises an amount of the mucin peptide conjugated to an immunogenic protein effective to stimulate or enhance immune response in the subject, together with an adjuvant and a vehicle. A cysteine is added to the N-terminal of this peptide to facilitate the conjugation with protein carriers. The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its derivative. The vaccine can be used to induce an immune response in patients suffering from a cancer of the type where the cancer cells have mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer, colon cancer or pancreas cancer.
                                                                                                                                                                                                                                                                                                                                                                  This mucin peptide is used in a vaccine capable of producing an immune
                                                                                                                                                                                                             Vaccine effective against cancer of the breast, prostate, colon, lung or pancreas - comprising mucin peptide, especially MUC1, conjugated to immunogenic protein, especially keyhole limpet haemocyanin
                                                                                               (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 11; 45pp; English
                97WO-US04493.
                                                       96US-0013775.
                                                                                                                                       Zhang S;
                                                                                                                                                                                WPI; 1997-480158/44.
                                                                                                                                       Livingston PO,
                20-MAR-1997;
                                                       20-MAR-1996;
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51 AA; Sequence

3; 1 TSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 55 -----ppahgvt 43 Query Match 17.2%; Score 52; DB 18; Length 51; Best Local Similarity 36.4%; Pred. No. 1.1e+02; Matches 20; Conservative 3; Mismatches 18; Indels 14; õ g

Search completed: July 13, 2001, 17:40:58 Job time: 175 sec

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LENGTH: 15 amino acids TYPE: amino acid
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15 HLPQPVSTRSQHTQP 29
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COMPUTER READABLE FORM:
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Matches 15; Conserv
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Query Match
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RESULT
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/cgn2_6/ptodata/3/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-483-432-19
US-08-471-780C-44
US-08-467-282B-44
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Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 57
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Maximum DB seq
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Sequence 53, Appl
Sequence 39, Appl
Patent No. 5171685
Patent No. 518916
Sequence 37, Appl
Sequence 29, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 11, Appl
Sequence 13, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
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  PCT-US95-04018-53
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US-08-812-829-29
PCT-US92-10432-1
US-08-65-469-43
542249-4
US-08-65-469-43
US-08-85-469-43
US-08-85-469-43
US-08-86-591-15
US-08-36-591-15
US-08-386-591-15
US-08-36-9354-1
US-08-361-920-13
US-08-361-920-13
US-08-443-432-13
US-08-443-432-13
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                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56, Application US/08221583 Patent No. 5486595 GENERAL INFORMATION:
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100.0%; Pit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      E: Floppy disk
IBM PC compatible
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.....TERISTICS:
TYPE: amino acids
TOPOLOGY: 1**
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Best Local Similarity 100.
Matches 15; Conservative
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ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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FILING DATE: 01-APR
                                                           COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
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CLASSIFICATION:
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.5%; Score 83; DB 5; Length 15; 100.0%; Pred. No. 0.0034;
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                         Tumor Necrosis Factor Inhibitors
                                                                                                                                   NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: Norris
                                                                                                                                                                                                                           STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
Sequence 56, Application PC/TUS9504018 GENERAL INFORMATION:
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100.0%; Pit
                                                       APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
                                        : Heavner, George A
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Best Local Similarity 100.
Matches 15; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-221-583-58
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                                    APPLICANT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relase #1.0, Version #1.25:mdctcMod
CURRENT APPLICATION DATA:
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APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Moodcock Washburn Kurtz Washb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 1; ; Pred. No. 0.0044; 0; Mismatches 0;
                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELEFOHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46th Floor
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APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US 08/221,581
01-APR-1994
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PCT-US95-04018-58

Sequence 58, Application PC/TUS9504018

Sequence 18, Application PC/TUS9504018

Sequence 18, Application PC/TUS9504018

Sequence 18, Application PC/TUS9504018
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Ponsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                Sequence 62, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INFORMATION:
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Deluca, Mark
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: CCR-0185
RELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3400
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pi
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APSTSFLLPMGPSPP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 APSTSFLLPMGPSPP 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pennsylvania
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RESULT 6
US-08-221-583-62
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                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsvlvania
                                                                                                                                                                                                                                                                                                                                     ;
0
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0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                          Score 82; DB 5; Length 15;
Pred. No. 0.0044;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.8%; Score 81; DB 1; Length 15; 100.0%; Pred. No. 0.0055; Live 0; Mismatches 0; Indels
                                      CCOR-0232
                                                                                                                                                                                                                                                                            27.2%; Sco.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/08221583 Patent No. 5486595
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NAME: Debuga, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
            REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids
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Matches 15; Conservative
                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-58
                                                                                                                                                                                                                                                                                                                                                                                              1 SQHTQPTPEPSTAPS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRSQHTQPTPEPST 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-221-583-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 STRSQHTQPTPEPST 35
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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APPLICANT: Heavne
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Gaps

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CURRENT APPLICATION DATA

Gaps

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APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Macklewicz & No. 5486595rls
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                             ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%; Score 80; DB 1; Length 15; 100.0%; Pred. No. 0.0071; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                    26.8%; Score 81; DB 5; Length 15;
100.0%; Pred. No. 0.0055;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                            CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
                   NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 amino acids
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                    linear
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 19403
                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. nc.
                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/221,583
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
ATTORNEY AGENT INFORMATION:
NAME: DeLUCA, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
APPLICATION NUMBER: PCI/US95/04018
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
PCT-US95-04018-62
Sequence 62, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide PCT-US95-04018-57
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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  Sequence 59, Application US/08221583
Sequence 59, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavure, George A.
TITLE OF INVENTION: Tunor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Pennsylvania
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.5%; Score 80; DB 1; Length 15; 100.0%; Pred. No. 0.0071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hearner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Mobert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Noodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Noris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Penalyvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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PCT-US95-04018-55
Sequence 55, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MAIK
RECISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-08-221-583-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 TOPTPEPSTAPSTSF 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                    19403
US-08-221-583-59
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Pred. No. 0.0071;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.5%; Sco...
100.0%; Pred. No. ...
0; Mismatches
         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
REJESTRATION NUMBER: 33,229
REFERENCE/POCKET NUMBER: 33,229
REFERENCE/POCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 55:
CFOTHENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
  PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19403
COMPUTER READABLE FORM:
MEDLIN TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
PT-1059-74018-59
Sequence 59, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Heavner, George A. APPLICANT: Kruszynski, Marian APPLICANT: Mervlc, Miljenko APPLICANT: Weber, Robert W. TITLE OF INVENTION: Tumor Necr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.5
Best Local Similarity 100.
Matches 15; Conservative
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MOLECULE TYPE: peptide
PCT-US95-04018-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAVHLPQPVSTRSQH 15
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CORRESPONDENCE ADDRESS:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Meric, Miljenko
APPLICANT: Meber, Nobert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                 STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORTGPETFGCT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                                            Sequence 61, Application PC/TUS9504018
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            Pennsylvania
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04018-61
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                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
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3. 0.0071;
0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No
                                                                                                                                                                                                                                                                                                                              26.5%; Scc...
100.0%; Pred. No. v...
0; Mismatches
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NAME: Debuga, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                   NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.2%; but
100.0%; Pre
0;
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                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
FILING DATE: 01-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 amino acids
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US95-04018-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TQPTPEPSTAPSTSF 15
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CLASSIFICATION: 514
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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Gaps
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Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 5; Ler
Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.2%; Sco. 100.0%; Pred. No. v. 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DAME: US 0A.APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
APPLICATION NUMBER: US 08/221,583
FILING DAME: US 0A.APR-1994
ATORNEY AGENT INFORMATION:
NAME: DeLUCA, MARK: DELCATON NUMBER: US 08/221,581
FREJENGALCA, MARK: NAME: DELCATON NUMBER: US 08/221,581
TELECOMMUNICATION NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 amino acids
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Matches 15; Conservative
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1 PSTAPSTSFLLPMGP 15

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31 PSTAPSTSFLLPMGP 47

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STREET: One Liberty Place 46th Floor

CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
COUNTRY: USA
COMPUTER: Pennsylvania
COMPUTER: ELBAPE. FORM:
MEDIUM TYPE: BAPEC. COMPUTEN: LBM PC COMPUTEN: LBM PC COMPUTEN:
COMPUTER: LBM PC COMPUTEN: BAPELICATION DATE:
COMPUTER: Patentin Release #1.0, Version #1.25:mdctcMod.
SSOFTWARE: Deluca, Mair:
APPLICATION NUMBER: US/08/221,583
FLIANG DATE:
CLASSIFICATION NUMBER: 33,229
REFERENCE/COCKET NUMBER: 33,229
REFERENCE/COCKET NUMBER: 33,229
REFERENCE/COCKET NUMBER: 33,229
RELEPRATION NUMBER: 33,229
RELEPRATION SOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid
TYPE: Amino ac
```

Search completed: July 13, 2001, 17:41:37 Job time: 169 sec

9 9

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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protein - protein search, using sw model S

July 13, 2001, 17:43:23 ; Search time 13.27 Seconds (without alignments) 321.460 Million cell updates/sec Run on:

US-09-800-909-2\_COPY\_202\_257 297 Title: Perfect score:

STSPTRSMAPGAVHLPQPVS.....STSFLLPMGPSPPAEGSTGD Sequence:

26

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues

Searched:

of hits satisfying chosen parameters: Total number

DB seq length: 0 DB seq length: 56 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mucin, qallbladder	hypothetical prote			arabinogalactan pr		MHC class I HLA-J	sepiapterin reduct	1 5	11 Iq	gen alpha		troponin T 2fa - r	H+-transporting AT	H+-transporting AT	extensin - tomato	mucin - sheep (fra	neural cell adhesi	etica	1 prote	gp18 protein - Myc	hetical p		H+-transporting AT	myosin catalytic l	aspartate transcar	hypothetical prote		serpin I - horse (
SUMMARIES	Ð	272	332	900	140692	S07073	T36022	156139	S32108	D81737	154515	A46662	A37172	I46522	S08424	T11184	T07030	A29789	G39690	H64801	A33756	G72801	S58216	T11131	T11105	S01945	S51176	C81117	S23202	S14338
	DB	7	~	7	~	~	7	7	7	7	7	7	~	7	7	7	7	~	7	7	N	N	~	~	~	~	~	~	~	7
	Length		52	42	25	46	31	28	47	54	31	39	36	48	52	55	43	20	29	20	51	51	52	24	55	52	27	51	23	54
dР	Query	, e	o,	8	•	16.8	υ.	•	14.6	4	14.5	4	4	14.1	14.1	4.	'n	e,	13.5	m.	ω.	е Э	•	ω.	ë.	٠	ë.	13.0	2	12.8
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	Result No.	-	7	m	4	S	9	7	œ	σ	10	. 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

55 2 \$29770 55 2 \$437238 51 2 \$25433 51 2 \$25433 51 2 \$25433 52 2 \$260 53 2 \$7213 51 2 \$82040 55 2 \$12040 55 2 \$1412 56 2 \$74112 57 2 \$17672 57 2 \$17672	DNA-binding protei	neural cell adhesi	hypothetical prote	hypothetical 3K pr		Ig alpha chain, tr	beta-fructofuranos	dihydrolipoamide S	hypothetical prote	hypothetical prote	hypothetical prote	proline-rich antib	neural cell adhesi	unknown protein en	hypothetical prote
	S29770 A37238	S25433	T29481	JC1360	S68260	S24713	S72213	B32040	A82795	S17805	C72610	S74112	139690	E85716	S17672
	0.0	~	۲۵	•	•	•	•	7	7	7	•		•	α	63
										_		_	_		
	12.8	12.6	12.6	12.5	12.	12.5	12.5	12.5	12.5	12.3	12.3	12.1	12.	12.	12.
38 12.8 37.5 12.6 37.5 12.6 37.5 12.6 37 12.5 37 12.5 37 12.5 37 12.5 36.5 12.3 36.5 12.3 36.5 12.3 36.5 12.3 36.5 12.3	<b>60 60</b>				37 12.5	37 12.5	37 12.5	37 12.5	7			ဖ	<sub>o</sub>		

## ALIGNMENTS

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           mucin, gallbladder - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                         1 STSPIRSMAPGAVHLPQPVSTRSQHT-QPTPEPSTAPSTSF---LLPMGPSPPA 50
                                                                                                                                                                                                                                                             25; Indels
                                                                                                                                                                                                                           Query Match 23.9%; Score 71; DB 2; Best Local Similarity 35.2%; Pred. No. 2; Matches 19; Conservative 6; Mismatches 2:
A60726
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A;Cross-references: EMBL:271614; NID:91302466; PID:e239576; PID:91302467; GSPDB:GN000 A;Experimental source: strain S288C C;Species: Saccharomyces cerevisiae C;Date: 27-Apr.1996 #sequence\_revision 03-May-1996 #text\_change 05-Nov-1999 C;Accession: S63324 R;Obermaler, B; Piravandi, E.; Rinke, M. submitted to the Protein Sequence Database, April 1996 A;Reference number: S63317 hypothetical protein YNL338w – yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein N0170 A; Molecule type: DNA A; Residues: 1-52 <OBE> C; Genetics: A; Gene: MIPS: YNL338w

20; Indels 7 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP Score 56.5; DE Pred. No. 38; 4; Mismatches 19.0%; ilarity 35.7%; Conservative Query Match Best Local Similarity Matches 15; Conserv ò

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Gaps

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Length 52;

DB 2;

A; Map position: 14L

RESULT

A; Molecule type: DNA A; Accession: I70082

Query Match

Best Loca Matches

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C: Keywords: hydroxyproline F:6,7,9,11,14,16,18,20,26,30,34,36,39/Modifled site: hydroxyproline (Pro) *status exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rimeser, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Weiss, E.H.; Girdlestone, J. J. Immunol. 148, 4043-4053, 1992
A;Title: HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Imp A;Reference number: 156139; MUID:92291530
A;Accession: 156139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I56139; I72807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 24/3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A;Accession: 172807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-28 <RE2>
A;Cross-references: GB:M80469; NID:g188483; PIDN:AAA36307.1; PID:g188484
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0
                                                                                                                                                                                                                                                                                                                                                                                                                               small hypothetical protein SCC54.09c - Streptomyces coelicolor
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                                                                                                            Length 46;
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Pred. No. 1.6e+02;
5; Mismatches 10;
                                                                                                         Score 50; DB 2; Le
Pred. No. 1.3e+02;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 44; DB 2; Le
40.9%; Pred. No. 2.6e+02;
tive 3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                              16 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain A3(2)
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                                                                                                      Query Match
Best Local Similarity 37.1%;
Matches 13; Conservative
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A;Accession: T36022
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Best Local Similarity
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A;Gene: SCOEDB:SCC54.09c
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Matches 9; Conserv
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A; Residues: 1-28 <RES>
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T36022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cenA protein (IgAlh) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession: 14069.
R;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warrer FEMS Microbiol. Lett. 92, 199-204, 1992
A;Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arabinogalactan protein - Italian ryegrass (fragments)
C;Species: Lolium multiflorum (Italian ryegrass)
C;Species: Lolium multiflorum (Italian ryegrass)
C;Date: 21.Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C;Accession: S07073
R;Gleeson, P.A.; McNamara, M.; Wettenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem, J. 264, 857-862, 1989
A;Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-A;Reference number: S07073; MUID:90147544
A;Reference number: S07073
A;Molecule type: protein
A;Residues: E-46 cGEE>
A;Note: 19-His and 23-Leu were also found
                                                                                                                                                                                                                  Ricopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A; Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-42 <RES>
A;Cross-references: GB:S34439; NID:g249178; PIDN:AAB22153.1; PID:g249179
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein C;Keywords: glycoprotein
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                                                                                                      glycoprotein Ib alpha variant B - human (fragment)
C;Species: Homo sapiens. (man)
C;Date: 02-4ug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I70082
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A;Residues: 1-25 <RES>
A;Cross-references: EMBL:X65780; NID:9312035; PIDN:CAA46663.1; PID:9312036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PTSEPAPSPT-TPEPTSEPAP-SPTTPEPTSEPAPS---PTTPEP 41
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: 140692
A;Accession: 140692
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SQHTQPTPEPSTAPSTSFLLPMGPSP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SVSTPPTPSPSTPPT-----PSP 19
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35.6%;
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mes 16; Conservative
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Best Local Similarity 46.2°
Matches 12; Conservative
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RESULT S07073

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Gaps

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C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1993 #Sequence_revision 18-Nov-1994 #text_change 28-Jul-1995
C;Accession: A46662
R;Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.
J. Biol. Chem. 268, 9381-9386, 1993
A;Title: Isolation and characterization of the chains of type V/type XI collagen pres
A;Reference number: A46662; MUID:9352802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-39 <MAY>
A;Residues: 1-39 <MAY>
A;Residues: 1-39 <MAY>
A;Nore: sequence extracted from NCBI backbone (NCBIP:131547)
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASTULT 12
A37172
Collagen alpha 1(XII) chain-like, skin and tendon - bovine (fragments)
Collagen alpha 1(XII) chain-like, skin and tendon - bovine (fragments)
Collages: Bos primigenius taurus (cattle)
Collages: Jan-1992 #sequence_revision 31-Jan-1992 #text_change 19-oct-1995
Collages: A37172
R.Dublet, B.; Van Der Rest, M.
Ann. N. Y. Acad. Sci. 580, 436-439, 1989
Astille: Comparison between chicken type XII collagen and bovine homologues.
A;Reference number: A37172
                                                                 A;Cross-references: GDB:137325
A;Map position: 22q11.2-22q11.2
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 42; DB 2; Leuy....
41.4%; Pred. No. 5.1e+02;
......hag 8; Indels
                                                                                                                                                                                                                                                          Length 31;
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53.3%; Pred. No. 4.5e+02;
Live 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                          Score 43; DB 2;
Pred. No. 3.5e+02;
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C; Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 OPKTIPSVILELPSCEEPOANKAI 25
                                                                                                                                                                                                                                                                                                                                                                                                                31 EPSTAPSTSFLLPMGPSPPAEGST 54
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-36 <DUB>
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Matches 8; Conserv
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                                      A; Gene: GDB: IGLL2
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C;Genetics:
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: TM1-2000 #sequence_revision 31-Mar-2000 #text_change l1-May-2000
C;Accession: D81737
R;Read, T.D.: Brunham, R.C.; Shen, C.; G111, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:2015025
A;Accession: D8173
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <TETP
A;Cross-references: GB:AE002280; GB:AE002160; NID:97190162; PIDN:AAF39005.1; PID:9719016
C;Genetics:
A;Gene: TC0127
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                                                                                                                                                                 Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musurulus (house mouse)
Cispecies: 382108
A.R. Maier, J.
Submitted to the EMBL Data Library, March 1993
A.Reference number: 332108
A.R. Status: preliminary
A.R. Status: preliminary
A.R. Status: preliminary
A.R. Status: 1-47 cMRA
A.R. Status: 1-47 cMRA
A.R. Residues: 1-47 cMRA
A.R. Coss.references: EMBL: 221947
C.R. Status: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.6%; Score 43.5; DB 2; 39.3%; Pred. No. 4.9e+02; Live 3; Mismatches 13;
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42.9%; Pred. No. 5.7e+02;
tive 5; Mismatches 10;
                                                                                                                                                      - mouse
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Length 55; Indels

DB 2; Leny .7.9e+02; 5;

Score 42; DB 3 Pred. No. 7.9e-1; Mismatches

14.1%; 52.4%;

49

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A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                         A; Cross-references: EMBL: AF090340; NID: 94894488; PID: 94894493; PIDN: AAD32518.1
C; Genetics:
                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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Job time: 106 sec
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Best Local Similarity 52.49
                                                                                                           A; Molecule type: DNA
A: Residues: 1-55 <MIN>
                  A; Accession: T11184
                                                                                                                                                A; Residues:
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C;Accession: 146522
B;Biggs, M.M.: Lin, J.J.; Schachat, F.H.
J; Muscle Res. Cell. Motil. 8, 1-12, 1987
A;Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle trope A;Reference number: 146522; MUID:87251333
A;Accession: 146522; MUID:87251333
A;Accession: 146522
A;Accession: A;Accession: A;Accession: A;Accession: Compared from GB/EMBL/DDBJ
A;Mccule type: mRNA
A;Mclecule type: mRNA
A;Mcscule type: mRNA
A;Mcscule type: mRNA
A;Cross-references: EMBL:U04975; NID:9440810; PIDN:AAA16028.1; PID:9440811
C;Superfamily: troponin T
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A), residues: ERBL:X17659; NID:g14006; PIDN:CAA35655.1; PID:g14007
R; Johansen, S.; Bakke, I.
R; Johansen, S.; Johansen, J.
R; R; Johansen, S.; Johansen,
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Till84
+-transporting ATP synthase (EC 3.6.1.34) protein 8 - Smithornis sharpei mitochondrion C; Species: mitochondrion Smithornis sharpei C; Accessian: Till84
R; Mindell5, D.P.; Sorenson, M.D.; Dimcheff, D.E.
Proc. Natl. Aprid Sci. U.S.A. 95, 10693-10697, 1998
A; Title: Multiple independent origins of mitochondrial gene order in birds.
A; Reference h; Muber: 217242
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A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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S08424
H-transporting ATP synthase (EC 3.6.1.34) protein 8 - Atlantic cod mitochondrion (Species: mitochondrion Gadus morbua (Atlantic cod)
C.Species: mitochondrion Gadus morbua (Species: 29-Jan-1993 #text_change 20-Jun-2000
C.Species: mitochondrion 29-Jan-1993 #text_change 20-Jun-2000
R.Johansen, S.; Guddal, P.H.; Johansen, T.
Nucleic Acids Res. 18, 411-419, 1990
A;Title: Organization of the mitochondrial genome of Atlantic cod, Gadus morbua.
A;Reference number: S08424; MUID:90174958
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6.8e+02;
9; Indels
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Pred. No. 7.9e+02;
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A; Residues: 1-55 <JOH>
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July 13, 2001, 17:44:53 ; Search time 9.89 Seconds (without alignments) 193.964 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                             93435 segs, 34255486 residues
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ATP8_PAROL
FOR2_MYRGU
YPU3_RHOCA
ATP8_SQUAC
CA11_RABIT
ATP8_SALAL
FOR1_MYRGU
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ATP8_LOXNO
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ATP8_CARAU
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4 55 1 ATPB_AYTAM 55 1 ATPB_CROLA 50 1 PENI_PERVA 50 1 PENI_PERVA 51 1 A70A_DROSE 52 1 A70A_DROSE 53 1 A70A_DROSE 54 1 ENI_ENSMI 55 1 A70A_DROSE 56 1 CATG_RAT 57 1 HIS_STRPU 58 1 HIS_STRPU 59 1 HOCM_SOLTU 50 1 LAMA_EMENI 50 1 LAMA_EMENI	ALIGNMENTS	STANDARD; PRT; 52 AA. 1. 34, Created) 1. 34, Last sequence update) 1. 40, Last annotation update)	in cosi ir's yea Sacchai	[1] SEQUENCE FROM N.A. Obermaler B., Piravandi E., Rinke M.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases -! SIMILARITY: TO YEAST YHR217C.	This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities a license agreement (See http://www.isb.cor send an email to license@isb-sib.ch).	CAA96274.1;; CAA96273.1; 2; YNL338W. Protein. 2 AA; 5951 MW; C1E4066D43E057A1	19.0%; Score 56.5; 35.7%; Pred. No. 28 vative 4; Mismatche: STRSQHTQPTPEDSTAPSTSFLLI	NRD; PRT; 55 Created) Last sequence upda Last annotation up 8 (EC 3.6.1.34) (AI 1c cod). Chordata; Craniata;
34 31 100.336 30.5 100.337 30.5 100.338 30.5 100.338 30.5 100.40 30 100.41 30 100.44 3		EESULT 1 YN78_YEAST ID YN78_YEAST ST. AC P53820; DT 01-OCT-1996 (Rel. DT 01-OCT-1996 (Rel. DT 01-OCT-1996 (Rel. DT 01-OCT-1996 (Rel.	HYPOTHETICAL 6.0 KDA PROTEIN I YAL338W OR NO170. Saccharomyces cerevisiae (Bake Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomy NCBI TaxID-4932;	[1] SEQUENCE FROM N Obermaler B., P Submitted (MAY!-SIMILARITY:	This SWISS-PROT between the Sw the European Bl use by non-pr modified and th entities requir or send an emai	EMBL; Z71614; C EMBL; Z71613; C SGD; S0005282; Hypothetical pr	Query Match Best Local Similarity Matches 15; Conser 7 SMAPGAVHLPOPV 1   :::    11 SMQYSDIXIPPTPT	2 ADMO 1F8_GADMO 1-8PR-1990 (Re 1-APR-1990 (Re 1-CTT-2000 (Re TP SYNTHASE PR TATPB OR ATPB. adus morhua (A itochondrion. ukaryota; Meta
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                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP8_PELSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96414925; Pubmed-8817926;
Mediline-96414925; Pubmed-8817926;
Johansen S., Bakke I.;
"The complete mitochondrial DNA sequence of Atlantic cod (Gadus morhua): relevance to taxonomic studies among codfishes.";
Mol. Mar. Biol. Biotechnol. 5:203-214(1996).
-I- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBDINTY) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-I- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-I- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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  Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                    Johansen S., Guddal P.H., Johansen T.; "Organization of the mitochondrial genome of Atlantic cod, Gadus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 4 24 POTENTIAL.
SEQUENCE 55 AA; 6481 MW. mornal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 55;
Pred. No. 5e+02;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENE 18 PROTEIN (GP18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AA.
                                                                                          SEQUENCE FROM N.A.
STRAIN=NORWEGIAN COASTAL 1; TISSUE=Liver;
MEDLINE=90174958; PubMed=2308841;
                                                                                                                                                                                                                                        Nucleic Acids Res. 18:411-419(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 LPQPVSTRSQHTQPTPEPSTAPSTS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 LPPKVMAHIFPNEPSPQGMTTPKTA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98300335; PubMed=9636706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. M. Biol. 279:143-164(1998).
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32.0%;
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Best Local Similarity 32.0°,
-hea 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X99772; -; NOT_
PIR; S08424; S08424.
InterPro; IPR001421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-28369;
                                            NCBI_TaxID=8049;
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064211;
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VG18_BPMD2
AC 064211.
DT 15-DEC.
DC NYTUSE
OC NYTUS
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
NCBI_TaxID=44522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ;
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15-JUL-1999 (Rel. 38, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. TRANSMEM 4 24 POTENTIAL. SEQUENCE 55 AA; 6536 MW: DADARCRERGEIAAN; CANALLY CANALLY CONTRACTOR CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%; Score 40; DB 1; Length 55; 36.0%; Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
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                                                                                                                                                                                                                                                                                                                                                                               EF85B1AFF5786A34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1; ]
Pred. No. 6.9e+02;
4; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTATP8 OR ATP8.
Pelomedusa subrufa (African side-necked turtle)
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TAGP_HUMAN
TAGP_HUMAN
STANDARD; PRT; 56 AA
AC Q9Y3F1;
DT 01-0CT-2000 (Rel. 40, Created)
DT 01-0CT-2000 (Rel. 40, Last sequence update)
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InterPro; IPR001421; -.
Pfam; PF00895; ATP-synt_8; 1.
                                                                                                                                                                                                                                                                                                                                   EMBL; AF022214; AAC18458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.5%;
                                                                                                                                                                                                                                                                                                                                                                               5680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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Best Local Similarity
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FOR2_MYRGU P81437;
                                                                                                                                                                                                                              ATP8_PAROL
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 16:10037-10052(1988).
--- SUBUNIT: MYOSIN IS AN HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
--- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS PROTEIN DOES NOT BIND CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Promoter analysis of myosin alkali light chain genes expressed in mouse striated muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                          "A 56 aa polypeptide with phosphorylation motif, potentially associated with Tap2 isoform activity."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      -1- FUNCTION: MAY BE ASSOCIATED WITH TAP2 ISOFORM ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 56; Pred. No. 9.2e+02; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C3H; TISSUE-Spleen;
MEDLINE-89057447; PubMed-3194193;
Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
                                                                                                                                                                                                                                                                                                                               ACD5D233EEC2C3BA CRC64;
01-ďcr-2000 (Rel. 40, Last annotation update)
TAP2-ASSOCIATED 6.5 KDA POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AA
                                                                                                                                                                                                                                                                                                                EMBL; AF152583; AAD32715.1; -.
                                                                                                                                                                                                                                                                                                                                                                           13.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                 29 TPEPSTAPSTSFLLPMGPSP 48
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TPQILTISFVSYILSLFPSP 25
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HSSP; P04002; lATF.
                                                                                                                                                                                                                                                                                                                               56 AA; 6535 MW;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.1 Best Local Similarity 40.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                              Homo sapiens (Human)
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buckingham M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYL3 OR MLC1V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
MLEV_MOUSE
ID MLEV_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FRAGMENT)
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete nucleotide sequence of Japanese flounder mitochondrial genome: structural property and cue for resolving teleostean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygil; Percomorpha; Pleuronectilformes; Pleuronectoidel; Bothidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saitch K., Hayashizaki K., Yokoyama Y., Asahida T., Toyohara H., Yamashita Y.,
                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00895; ATP-synt_8; 1. Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. SEOUENCE 55 AA; 6571 MW; 2B5EFEZ0FDCB6AA9 CRC64;
                                                                                                                                      Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 55;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT
                                                                   CE513ECBA3C8258D CRC64;
                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1; 1
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                           5 РЕРККООАКАААРКААРААРААРАААРВАВЕРЕКРКЕ 42
                                                                                                                                      Score 38; DB 1;
Pred. No. 1e+03;
                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                  16 PQPVSTRSQHTQP--TPEPSTAPSTSFLLPMGPSPPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 55 AA
                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
Myosin; Muscle protein; Multigene family.
INIT_MET 0 0 0
NON_TES 5.1 5.1
SEQUENCE 5.1 AA; 5085 MW; CE513ECBA3CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 LPQPVSTRSQHTQPTPEPSTAPST 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 IPPKVLAHTFPNEPTPQSTQKPKT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB028664; BAA89037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (Rel. 40, Created)
                                                                                                                                      12.8%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%;
29.2%;
                                                                                                                                      Query Match 12.8
Best Local Similarity 26.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001421; -. InterPro; IPR003214; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTATP8 OR ATP8
                                                                                                                                                                                                                                                                                                                                                                                            ATP8_PAROL Q9T9D5;
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17 OPVSTRSQHTQPTPEPS--TAPSTSFLLPMGPSP-PA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                             MTATP8 OR ATP8
                                                                                                                                                                                                                          Mitochondrion
                                                                                                                      Q92250;
30-MAY-2000
                                                                                                                                                                01-OCT-2000
                                                                                                                                                   30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA11_RABIT
                                                                                                       ATP8_SQUAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                      Myrmecia gulosa (Red bulldog ant).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Formicoidea; Formicidae; Myrmecia.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
11-MAY-1992 (Rel. 22, Last annotation update)
11-MYPOTHETICAL 5.8 KDA PROTEIN IN PUHA 5'REGION (ORF55).
11-MYPOTHETICAL 5.8 KDA PROTEIN (Rhodopseudomonas capsulata).
11-MAY-1992 (Rhodopseudomonas capsulata).
11-MAY-1992 (Rhodopseudomonas capsulata).
11-MAY-1992 (Rhodopseudomonas capsulata).
                                                                                                                                                                                                                                                                                             -1- INDUCTION: UPON BACTERIAL CHALLENGE.
-1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE,
GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
-1- SIMILARITY: TO DROSOPHILA DROSOCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 37.5; DB 1; Length 16; 47.1%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.5; DB 1; Length 55;
Pred. No. 1.5e+03;
2; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
CARBOHYD 11 11 0-LINKED (GALNAC. . .).
SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                                SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
(Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 PQPVSTRSQHTQPTPEP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PNPVNTK----PTPYP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z11165; CAA77517.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 47.1 tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.3
Best Local Similarity 40.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S17805; S17805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photosynthesis;
15-DEC-1998 (
15-DEC-1998 (
30-MAY-2000 (
                                            FORMAECIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPU3_RHOCA
P26159;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasmussen A.S., Arnason U.;
"Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes.";
U. Mol. Evol. 48:118-123(1999).
-: FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-: SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-: SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
8
                                                                                                                                                                                                                                                                       OCT-2000 (Rel. 40, Last annotation update)
SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
3FB9F843CEFA54EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Pred. No. 1.6e+03; 2; Mismatches 12
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-1995 (Rel. 32, Last annotation update)
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).
                                                                                                                                                           55 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA
                                                                                                                                                                                                                 (Rel. 39, Created)
(Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VHLPQPVSTRSQHTQPT-----PEPSTAPST 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VILPKKVMTHLFNNNPTAKSAEKPKPEPWNWPWT
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                         Squalus acanthias (Spiny dogfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-99091711; Pubmed-9873084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=70252720; Pubmed=4194291;
Bornstein P., Nesse R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y18134; CAA77053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AA; 6587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.1
Best Local Similarity 35.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA11_RABIT
1D CA11_R
AC P02456
DT 21-JUL
DT 21-JUL
DT 01-NOV
DE COLLAG
GN COLLAG
GN COLLAG
OC BURATY
OC MAMMAI
CO MAMMAI
RN [1]
RN [1]
RN SEGUEN
RA MEDLIN
RA BOINST
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NCBI_TaxID-8797;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                              FOR1_MYRGU P81438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMAECIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP8_RHEAM
079396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
ATP8_RHEAM
                                                                                                                                                                                                                                                                                                                                                                                                             FOR1_MYRGU
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                SERVE
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-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONEWZYMATIC COMPONENT (CF(0) SUBMIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome
                                                                                                                                                                                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. A02856; CGRB1S.
                                                                                                                                                                                                                                                                                                                                                                                                           CONVERTED TO AN ALDEHYDE GROUP THAT IS
                                                                                                                                              SUBUNIT: TRIMERS OF ONE ALPHA 2(1) AND TWO ALPHA 1(1) CHAINS. TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
           comparative biochemistry of collagen: the structure of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                          InterPro; IPR001007; -.
PROSITE; PS01208; VWFC; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doiron S., Blier P.U., Bernatchez L.;
"A comparative analysis of complete sequence of mitochondrial between brook char (Salvelinus fontinalis) and arctic char (S.
"The comparative biochemistry of collagen: the structure of r_i skin collagen and its relevance to immunochemical studies of
                                                                           Arch. Blochem. Blophys. 138:443-450(1970).
-!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
(FIBRILLAR FORMING COLLAGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                            INVOLVED IN CROSS-LINKING.
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
HYDROXYLATION (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROXYLATION (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127582E5E52B87FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VSVPGPMGPSGPRGLPGPPGAPGP2-GFZGPPG-ZPGZPGSSG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; I
Pred. No. 1.9e+03;
; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salvelinus alpinus (Arctic char).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4987 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTATP8 OR ATP8 OR ATPASE8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 13; Conserv
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                                                                                                                                                                                                                  HYDROXYAPATITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion
                                                                                                                                                                                                                                                                                       PIR; A02856;
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Q9XN27;
                                                      collagen.
                                                                                                                                                                                                                                                                                                                                                                                   Collagen.
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NON_TER
SEQUENCE
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MOD_RES
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MOD_RES
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AC GANNY
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DT O10-OCT
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CO BURARY
CO BURARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myrmecia gulosa (Red bulldog ant).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Formicoidea; Formicidae; Myrmecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Hemolymph;
MEDLINE-98165787; PubMed-9497332;
MacKintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
MacKintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
MacLincon from an Myrmecia gulosa of two inducible
O-glycosylated proline-rich antibacterial peptides.";
J. Biol. Chem. 273:6139-6143(1998).
I- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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Archosauria; Aves; Palaeognathae; Rheiformes; Rheidae; Rhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
-!- SIMILARITY: TO DROSOPHILA DROSOFIN.
Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
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01-6CT-2000 (Rel. 40, Last sequence update)
01-6CT-2000 (Rel. 40, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
MIATPB OR ATP8 OR ATPASE8
EMBL; AF154851; AAD41389.1; -.
InterPro; IPR001421; -.
Pfam; PF00895; ATP-SYTL_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SEQUENCE 55 AA; 6455 MW; 71E430C2E346924A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34.5; DB 1; Length 16; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                     Length
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80CEA3AABBC2E0AE CRC64;
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                                                                                                                                                                                  Score 35; DB 1;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AA
                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                  11.8%;
30.0%;
                                                                                                                                                                                                                                                                                                                   | : :| | :: |: | | 30 GHIFTNEPTSQSTEKTKPEP 49
                                                                                                                                                                                                                                                                                         30
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41.28;
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                                                                                                                                                                                                                                                                                         11 GAVHLPOPVSTRSOHTOPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 41.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 PQPVSTRSQHTQPTPEP 32
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PNPVNNK-----PTPHP 14
                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
Matches 6; Conserv
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Search completed: July 13, 2001, 17:47:36 Job time: 163 sec
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001641, 09V1AA0;

001-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
MALE SPECIFIC SPERM PROTEIN MST84DC.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                           Sorenson M.D., Dimcheff D.E., Ast J.C., Yuri T., Mindell D.P.;
"Complete mitochondrial DNA sequences for five birds and a turtle.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZWATIC COMPONENT
(CF(0) SUBUNIT) OF THE MITOCHOMDRIAL ATPASE COMPLEX.
-: SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-: SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                       MEDLINE-98272735; PubMed-9608049;
Harlid A., Janke A., Arnason U.;
"The complete mitochondrial genome of Rhea americana and early avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A cluster of four genes selectively expressed in the male germ line of Drosophila melanogaster.";
Mech. Dev. 35:143-151(1991).
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Adam's M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane. SEQUENCE 55 AA; 6493 MW; CF394C4267956648 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-OREGON-R;
MEDLINE-92102953; PubMed=1684716;
Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
Schaefer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 55;
Pred. No. 2.4e+03;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 HLP--QPVSTRSQHTQPTPEPSTAPST 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 NLPSNKPLST-----PNPTPWTWPWT 55
                                                                                                                        J. Mol. Evol. 46:669-679(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y16884; CAA76505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00895; ATP-synt_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.4%;
Best Local Similarity 40.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF090339; AAD32506.1;
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SEQUENCE FROM N.A.
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                                                                                                    divergences.";
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M84C_DROME
DAC 00164_M
A0164_M
DT 01-JUL-
DT 02-JUL-
DT 01-JUL-
DT 
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA burbin K.J., Evangelista C.C., Ferraz C., Ferriars S., Felsformann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriars S., Felsformann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.F., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.F., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J., Lin X.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Li S., Liang Y., Lin X.,
RA Martulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Diagon R., Pittman G. S., Pan S., Pollard J., Puri V., Rese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Yao Q. A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Williams S.M., Woodage T., Wenter J.C.,
RA Hang Z.H., Shortey E., Wassarman D.A., Weinstook G., Mu D., Yang S., Yao Q. A.,
RA Hanga C., Zhan M., Zhong W., Worley E., Wan S., Zhan M., Strong W., Shith H.O.,
Rhence S. R., Zhong F.N., Zhong W., Worley E., Shith H.O.,
R., Sheng R.N., Rocheller E., Spradling A., Rubert J. S., Zhan M., Strong W., Shith H.O.,
R., Sheng R.N., Shortey E.W., Rubert J. S., Shith H.O.,
R., Sheng R.N., Rubert B., Rubert J., Shiff-Juber B., Shith H.O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@libersib.ch).
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Pred. No. 2.4e+03;
); Mismatches 15; Indels
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FlyBase; FBGNO04174; Mst84Dc.
Spermatogenesis; Repeat; Multigene family.
SEQUENCE: 55 AA; 5225 MW; 95A12F3AEC88BD6C CRC64;
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Best Local Similarity
Matches 9; Conserv
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014069 homo sapien 079966 mogurnda ad 071179 chlamydomon 09h3t0 homo sapien 09h3t0 homo sapien 09h3t0 human respi 092309 human respi 092310 human respi 092310 human respi 092310 human respi 094169 human respi 094169 human respi 09541 bovine herp 092307 human respi 09541 bovine sapien 090990 oryctolagus 09mys0 oryctolagus 091829 homo sapien 09mys0 oryctolagus 092317 human respi

Q9wtu8 rattus norv bos taurus 3 human respi 092308 human respi

Total number of

Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Database

Q29321 sus scrofa

09udg4 homo sapten 09h134 homo sapten

us-09-800-909-2\_copy\_202\_257.rspt

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last sequence update)
Last annotation update)
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Last annotation update)
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Q9H3T0
Q9JFE6
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O61039
Q31629
Q9MYS0
Q29163
Q92317
Q29321
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
              Best_Local Similarity 35.6
Matches 16; Conservative
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NCBI_TaxID=9606
44
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092302 human respi
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0958800 solanum tub
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Q9g138 bos taurus
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                           hits satisfying chosen parameters:
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297
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Score

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STRAIN=181691;
Cogglas W.B., Lefkowitz E.J., Sullender W.M.;
Cogglas W.B., Lefkowitz E.J., Sullender W.M.;
Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (ANG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARG08872; ARC42992.1;
InterPro; IPR000925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=203721;
Coggins W.B., Lefkowitz E.J., Sullender W.M.;
"Genetic Variability among Group A and Group B Respiratory Syncytial
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                             Score 51; DB 14; Length 52;
Pred. No. 79;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008688; AAC43008.1; -.
InterPro; IPR000925; -.
                                                                                                                                                                                                                7C3114ACA02574E6 CRC64;
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5554 MW; 3B328FBC5B4E9858 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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(FRAGMENT).
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Pred. No. 79;
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5613 MW;
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31.8%;
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Best Local Similarity
Matches 14; Conserv
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NCBI_TaxID=11250;
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     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Paramyxovįridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                                                829FBEB4792EA30F CRC64;
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Pred. No. 62;
4; Mismatches 19;
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NCBI_TaxID=11250;
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; Pred. No. 26;
. 6; Mismatches
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                                                                                                                                                                                PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                              Submitted (JUL-1995) to the E
EMBL; L39103; AAA69491.1; -.
InterPro; IPR002965; -.
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34.3%;
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nilarity 35.6%;
Conservative
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                52 AA;
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                                                                                                 SEQUENCE FROM N.A
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SEQUENCE
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SEQUENCE
                                                                                                               Ishida F.
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092301;
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FCE1D38D8DEDC173 CRC64;
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Proc. Natl. Acad. Scl. U.S.A. 81:5561-5565(1984).
EMBL; K02578; AAA36505.1; -.
                                                                                                                                                                                                                                      Score 50; DB 6;
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 4 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 36
                                                                                                                                                                                                                                                                                                                                                                                              19 PKHSSDTGSKHAPKEKAVSKSSEQPPSEKSTKP 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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01-0CT-2000 (TrEMBLrel. 15, C
01-0CT-2000 (TrEMBLrel. 15, 7)
01-0CT-2000 (TrEMBLrel. 15, 7)
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4592 MW;
                                                                                                                                                                                                                                      16.8%;
illarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 16.7%;
Best Local Similarity 32.7%;
Matches 16; Conservative
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simian virus 40 (SV40).
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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46 AA;
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SEQUENCE
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                                             SEQUENCE FROM N.A.

MEDLINE=96326790; PubMed=8766138;

MEDLINE=96326790; PubMed=8766138;

MEDLINE=96326790; PubMed=8766138;

Sequence analysis of the GAG triplet repeats region in the Huntington disease gene (TT15) in several mammalian species.";

Ann. Genet. 39:81-86(1996).

EMBL; S83377; ABB50771.1; -.

NON_TER 1

SEQUENCE 33 AA; 3393 MW; 44F558CE5636722A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Teichert A.M., Karantzoulis-Fegaras F., Wang Y., Mawji I.A., Bei X., Gnanapandithen K., Marsden P.A.; "Characterization of the murine endothelial nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                    11;
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2
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                                                                                                                                                                                                                                                                                                                                                 Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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EMBL. AF091262; AAD22613.1; -.

NON_TER 54 54 54

SEQUENCE 54 AA; 5193 MW; IDA456A21958B2EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CALPASTATIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                              DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                               15 LPQPVSTRSQHTQP-TPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AA
                                                                                                                                                                                                                                                                                                                                            17.0%; Score 50.5; 38.5%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99096466; PubMed-9878824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 PTPEPSTAPSTSFLLPMGPSPPA 50
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Best Local Similarity 38.55
Matches 15; Conservative
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SEQUENCE FROM N.A.
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NCBÍ_TaxID=9595;
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Gaps
Chung H.Y., Davis M.E., Hines H.C.;
"PCR-SSCP analysis of the bovine calpastatin gene domain L region.";
"Davis Manalysis of the EMBL/GenBank/DDBJ databases.
EMBL; AY008267; AAG23869.1; -.
NON_TER 1 1
NON_TER 52 52
SEQUENCE 52 AA: 5749 MW; CBD5A7449AFDDA89 CRC64;
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Azen B.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
"Clones from the human gene complex coding for salivary proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
NCBI_TaxID=10633;
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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STRAIN-MC-028863B-1;
Rizzo P., Carbone M.;
Rizzo P., Carbone M.;
Sv40 from 1955 commercial parenteral (Salk) poliovaccine.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF180738; AAF28272.1; -.
SEQUENCE 54 AA; 5868 MW; 556CDAB682CIEFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.5; DB 14; Length 54;
Pred. No. 1.2e+02;
5; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SMAPGAVHLPQP-VSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 54
                                                                                                                                                                                                                                                                            6; Length 52;
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Last annotation update)
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InterPro; IPR000925; -.
Pfam; PF00802; Glycoprotein_G; 1.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 14; Conserv
                                                                                                52 AA;
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NON_TER
SEQUENCE
                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                 Query Match
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092303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.; ^{\rm A} new repetitive sequence uniquely present in the decay-accelerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 47:246-255(1998).
-!- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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"Genetic Variability among Group A and Group B Respiratory Syncytial Viruses in a Children's Hospital.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AFQ86873; AAC42993.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i - SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.5%; Score 49; DB 6; Length 51; Best Local Similarity 28.9%; Pred. No. 1.3e+02; Matches 13; Conservative 6; Mismatches 22; Indels
                                                      Length 46;
                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 PGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ED112B05C37548A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
                                                 16.5%; Score 49; DB 4; 38.2%; Pred. No. 1.2e+02; iive 2; Mismatches 15
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                                                                                                                                                       STRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
MEDLINE-98099759; PubMed-9435343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 51
51 AA; 5545 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ABÓ03315; BAA22903.1;
Complement pathway.
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
                                                 Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
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SEQUENCE
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DT 01-NOV-
DT 01-CCT-
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OC VITUSE
OC PATACHN
NN (1)
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RR SEQUEN
RC STRAIN-
RC COGG IN
RT "GENÊT. T
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Gaps
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"Genetic Variability among Group A and Group B Respiratory Syncytial
Viruses in a Children's Hospital.";
Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF086874; AAC42994.1;
InterPro: IPR000925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.5%; Score 49; DB 14; Length 52;
31.8%; Pred. No. 1.38+02;
tive 4; Mismatches 26; Indels
                                                                                              Score 49; DB 14; Length 52;
Pred. No. 1.3e+02;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pirone D.M., Fukihara S., Gutkind S.J., Burbelo P.D., "SPECS, small binding proteins for CDC42 proteins."; J. Biol. Chem. 0:0-012000)
EMBL, AF286592; AAG17723.1;
                                                                                                                                                                                                                                 5 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 52
52 AA; 5542 MW; C2028FBC5B551270 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G17723.1; -. 4245 MW; 3B416F3C5ADF4E91 CRC64;
                    C2029E4C5B551270 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
ATTACHMENT GLYCOPROTEIN G (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                         16.5%; Scor.
31.8%; Pred. No. 1...
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  52 AA
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                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00802; Glycoprotein_G; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Cro
01-MAR-2001 (TrEMBLrel. 16, Las
01-MAR-2001 (TrEMBLrel. 16, Las
SIGNALING MOLECULE SPECI BETA.
52
5530 MW;
                                                                                                                                                14; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Man Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A., Peelman L.J.;

Peelman L.J.;

Integration of porcine chromosome 13 maps.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL: AF222917; AAG41130.1;
                                  œ
Ouery Match
16.2%; Score 48; DB 4; Length 38;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 6; Indels
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16.2%; Score 48; DB 6; Length 42;
Best Local Similarity 36.6%; Pred. No. 1.4e+02;
Matches 15; Conservative 2; Mismatches 14; Indels
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42 42
42 AA; 4677 MW; 78BDD867E66EF64F CRC64;
                                                                                                                                                                O9GKJ3;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VHLPQPVSTRS----OHTQPTPEPSTAPSTSFLLPMGPSPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 VHSPQQVDFRSVLAKKGTPKTPVPEKLP-----PPKPTTP 42
                                                                                  13 VEKPQPVSL-----PTPHPN--PKSSQLL 34
                                                             13 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLL 42
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NON_TER
SEQUENCE
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Q9GKJ3
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Search completed: July 13, 2001, 17:47:19 Job time: 166 sec

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July 13, 2001, 17:41:38 ; Search time 19.93 Seconds (without alignments) 170.343 Million cell updates/sec
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/SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT:*
/SIDS8/gcgdata/geneseg/genesegp/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221992
                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412676 segs, 60623988 residues
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297
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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1: /srnce
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

/SIDS8/gcgdata/geneseg/genesegp/AA1998.DAT:\*

/SIDS8/gcgdata/geneseg/genesegp/AA1997

					SOFTWARTES		
Result No.	Score	% Query Match	% Query Match Length DB ID	DB	ID	Description	
1	68.5	23.1	47	21	AAB56300	Human secreted pro	
7	99	22.2	. 49	19	AAW59911 ·	Amino acid sequenc	
ო	59	19.9	45	12	AAR15261	Linking B region #	
4	28	19.5	24	15	AAR49722	Sequence of a pept	
S	58	19.5	54	15	AAR49536	Camel Iq 2-heavy c	
9	56.5	19.0	41	20	AAY01285	Peptide encoded by	
7	55	18.5	46	20	AAW88522	Amphotropic hyperv	
80	55	18.5	52	22	AAB61193	Human INTERCEPT 21	
6	54.5	18.4	55	21	AAB42690	Human ORFX ORF2454	
10	54	18.2	21	6	AAP81606	Sequence of human	
11	54	18.2	36	21	AAY65289	Human 5' EST relat	

53.5         18.0         37         18         AAR37992         He avy chain hinge heavy chain hinge have chain hinge heavy chain hinge heavy chain hinge heavy chain hinge hinge in the last of last of the last of last	ALIGNMENTS  Tr  AAB56300 standard; Protein; 47 AA.  AAB56300;  AAB56300;  AAB56300;  AAB56300;  AAB56300;  AAB56300;  Human secreted protein; diagnosis; immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungiciale; ophthalmological; gene therapy; pathological condition; autoimmune disease; rhemmatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebral isohaemia; cerebrovascular disorder; andiogenesis; nervous system disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebral isohaemia; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; food additive; preservative.  Homo sapiens.  WO200070042-A1.  23-NOV-2000;  11-MAY-2000; 2000WO-USI2788.  13-MAY-1999; 99US-0134068.  (HUMA-) HUMAN GENOME SCI INC.  ROSEN CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE; Duan RD, Florence KA, Soppet DR;
	RESULT AAB56300 ID AAB56300 XX AC AAB56 XX AC AAB56 XX AC AAB56 XX AX BUT 13-M4 AU DOT XX AU DOT

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Gaps

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Length 49 19; Indels

DB 19;

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decomposes the alpha-1,3 glucoside bond of mutan. The mutanase enzyme is used in the method of the invention for prevention and removal of plaque and bacteria on teeth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New fungal (hemi)cellulose degrading enzymes – for prodn. of l1q. fuel gas and feed protein, have specified carbohydrate binding domain
                                                                                          This is the amino acid sequence of the mutanase enzyme PT box, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linking B region #8 derived from a (hemi)cellulose-degrading enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is one of 8 specified linking B regions which are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a cellulose- or hemicellulose-degrading enzyme and which are enriched in the amino acids Gly and/or Asn and/or Pro and/or Se and/or Thr and/or Gln. It can be incorporated in a fusion protein comprising a catalytic domain from a cellulase, e.g. a Bacillus endoglucanase, and a carbohydrate binding domain from a fungal endoglucanase. See also AAR15254-R15260.
                                                                                                                                                                                                                                                                                                                                                                   3 SPIRSMAPGAVHLPQPVSIRSQHTQPTPEPSTAPSTSFLLPMGPSPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                sptptptptptptptptptptptptptptptptptpt-----ptpp 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 avqipss-stsspvnqptststtststtssppvqpttps-gctae 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal A region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hastrup S;
                                                                                                                                                                                                                                                                           Score 66; DB
Pred. No. 4.3;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hjort CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 46; 73pp; English.
of plague and bacteria on teeth
                                             Claim 2; Page 5; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substrate;
cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR15261 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%;
37.8%;
                                                                                                                                                                                                                                                                         22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-DK00124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90DK-0001158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                           Query Match 22.2
Best Local Similarity 31.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO NORDISK A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Woldike HF, Hagen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CBD; hemicellulosic
Trichoderma reesei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-353766/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                         49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9117244-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR15261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  10
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AAR15261
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                                                                                                                                                                     The polynucleotide sequences given in AAC99818 to AAC99977 encode the human secreted proteins given in AAB5607 to AAB56362. Human secreted proteins given in AAB5607 to AAB56362. Human secreted control in a activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; ansotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The human secreted polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, and proteins or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The proteins can also be used to aid wound healing and epithelial cell proliferation, to painteen a pervent or prevent skin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proteins can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC99809 to AAC9817 and AAB56076 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                             Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition \,

    used for prevention and removal

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutanase enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.5; DB 21; Length 47; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 pvstlplgpsptpshtahpptpspptpxshpsxpsppatsss 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of the mutanase enzyme PT box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 PVSTRSQHTQPTPE----PSTAPSTSFLLPMGPSPPAEGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                               Disclosure; Page 1035; 1065pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoging a mutanase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59911 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-0284362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96JP-0314057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                  WPI; 2000-679828/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-474495/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteria; teeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP10201483-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches

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RESULT AAW59911

5

Gaps

5,

18;

DB 12; Length 45;

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Camelus dromadarius.
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                                                                                                             EP584421-A.
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY01285;
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                                           Region
                                                              Region
                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                               Sequence of a peptide which is part of the heavy (H) chain (CH3) of an
                                                                                                                                                                                                                                                                                                                                                          A novel immunoglobulin (Ig) is claimed which comprises two heavy (H) polypeptide chains sufficient for the formation of a complete antigen binding site or several such chains. The Ig is devoid of light (L) polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E. coli, by: cloning a DNA or cDNA sequence coding for the WH domain of an Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids; recovering the cloned fragment after amplification using a 5' primer contg. an Xho site and a 3' primer contg. the Spe site having the sequence in AAQ44383; cloning the recovered fragment is a vector; transforming host cells; and recovering the expression product of the VHH coding sequence. A nucleotide encoding the peptides in AAR49721-24 is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin; Ig; heavy chain; constant region; variable region; antibody engineering; IgG2; IgG3.
                                                                                                                                                                                                                                                                                                            Immunoglobulins devoid of light chains - also processes for their preparation, and protein and nucleotide sequence encoding them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camel Ig 2-heavy chain molecule (clone no. 72/79).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ipqpqpkpqpqpqpkpqpkpqpkpepectcpkcpapellg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58;
Pred. No.
                                                                                                            Immunoglobulin; heavy chain; Camelid
                     AAR49722 standard; peptide; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 65; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR49536 standard; peptide; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.5%;
Best Local Similarity 31.6%;
Matches 12; Conservative
                                                                                                                                                                                          93WO-EP02214
                                                                                                                                                                                                            92EP-0402326
93EP-0401310
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                        Hamers R;
                                                                                        Lmmunoglobulin (Ig).
                                                                                                                                                                                                                                         (CAST/) CASTERMAN C. (HAME/) HAMERS R.
                                                                                                                              Camelus dromedarius.
                                                                                                                                                                                                                                                                                          WPI; 1994-083195/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AA;
                                                                                                                                                                                                                                                                       Casterman C,
                                                                                                                                                                                        18-AUG-1993;
                                                                                                                                                                                                            21-AUG-1992;
21-MAY-1993;
                                                                                                                                                  WO9404678-A.
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                                                           22-AUG-1994
                                                                                                                                                                      03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                         AAR49722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR49536;
4
             AAR49722
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  RESULT
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Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein; RPRP; arabino-galactan protein; AGP; glycopeptide; internal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This 2-chain Ig molecule lacks any light chains. The Ig has e.g. improved solubility and aggregate much less than heavy chains d. 4-chain IgS. The Igs can be used normally for e.g. diagnosis, therapy, in vaccines, for isolation and purification of antigens and in the production of anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated immunoglobulin molecules devoid of light polypeptide chains - consisting of heavy polypeptide chains only, obtd. from Camelid serum, for use as antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                   "heavy chain variable region"
                                                                                                                                                   "heavy chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.5%; Score 58; DB 15;
31.6%; Pred. No. 29;
Live 3; Mismatches 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 ipqpqpkpqpqpqpkpqpkpepectcpkcpapellg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide encoded by HRGP gene cassette.
                                                 /note= "hinge region"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                        92EP-0402326
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                                                                                                                      41..54
/note=
                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                          (CAST/) CASTERMAN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-067061/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     (HAME/) HAMERS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casterman C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9903978-A1
                                                                                                                                                                                                                                                                                                                                                        21-AUG-1992;
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Gaps

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Indels

17;

DB 20; Length 46; 49;

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The present sequence is given in a specification relating to isolated human proteins designated INTERCEPT 217, INTERCEPT 297, TANGO 276, TANGO 292, TANGO 331 and TANGO 332. These proteins are useful as modulating agents or as targeting agents for developing agents to regulate cellular processes e.g. growth, proliferation, survival, differentiation and activity of human tissues. Diseases which can be diagnosed, prevented and treated by administration of these polypeptides, their nucleic acids and modulators include cancers, inflammatory discorders, cardiac disorders e.g. arrhythmia, and skin disorders e.g. provides, cardiac disorders e.g. arrhythmia, and skin disorders e.g. provides, cardiac caids encoding the isolated proteins can be used to express the proteins in a host cell in gene therapy applications.

Antisense molecules or ribozymes can be used to inhibit expression cof the proteins in target cells. Fragments of the nucleic acid molecules encoding the isolated proteins are used as hybridisation probes and as polymerase chain reaction (PCR) primers.
hypervariable polyproline (HP) region modified to include a heterologous protein or peptide. Retroviral vectors made targetable by modification of the HP region enable the delivery of desired genes to a variety of cell types. Unlike prior art modifications in the receptor binding region, the particle does not disrupt envelope structure to impair folding, processing, and incorporation of the envelope protein. The present sequence represents an amphotropic hypervariable polyproline region truncated peptide from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, INTERCEPT 217; INTERCEPT 297; TANGO 276; TANGO 292; TANGO 325;
TANGO 331; TANGO 332; cytostatic; antiinflammatory; antiarrhythmic;
antipsoriatic; gene therapy; cancer; inflammatory disorder;
cardiac disorder; arrhythmia; skin disorder; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human proteins are used for diagnosis, treatment and prevention of cancers, inflammatory disorders, cardiac disorders e.g. arrhythmia, and skin disorders e.g. psoriasis
                                                                                                                                                                                                                                                                                                                                                                                               13 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human INTERCEPT 217 cytoplasmic domain.
                                                                                                                                                                                                                                                                                                    Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser CC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61193 standard; Protein; 52
                                                                                                                                                                                                                                                                                                    18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-2000; 2000WO-US16658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirst SJ, Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-061966/07
                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200100638-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61193;
                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                          The invention relates to novel synthetic genes for plant gums. A new approach is described to the production of hydroxyproline-rich glycoproteins (HRGPS). repetitive proline-rich proteins (RPRPS) and arabino-galactan proteins (AGPS). Synthetic genes comprising a nucleic acid encoding the peptide (AAY01267) can be engineered for the production of repetitive glycopeptide modules in cells. The invention provided a new approach to the problem of producing plant gums that is not dependent on environmental factors and greatly simplifies the production of a variety of naturally occurring gums as well as designer
                                                                                                                                                                                                                                - of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a retroviral vector particle (RVP1), having a modified retroviral envelope polypeptide which includes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphotropic hypervariable polyproline region truncated peptide N-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * retroviral vector particle - has envelope polypeptide modified the hypervariable polyproline region to enable cell targeting
                                                                                                                                                                                                                         Novel synthetic gene designed from repetitive peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypervariable polyproline region; amphotropic gp70 protein; human cytomegalovirus; hCMV; retrovirus; envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%; Score 56.5; DB 20; 43.3%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 STRSQHTQPTPEPSTAPSTSFLLPMGPSPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strasppppsppppsppps---ppppspp 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW88522 standard; peptide; 46 AA.
                                                                                                                                                                                                                                                    hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOUTHERN CALIFORNIA
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     97US-0897556.
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                                                                                                                                                     WPI; 1999-132225/11
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                                                     (UYOH-) UNIV OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AA;
                                                                                                                                                                           N-PSDB; AAX27690
                                                                                                     Kielszewski MJ;
     21-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1998;
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Barnes TS;

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02-OCT-1990
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                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive, dermatological; immunosuppressive; antidialematory; antidanemic; gene therapy; cancer; proliferative disorder; hypotenension; neurodegenerative disorder; proliferative disorder; hypotenension; cardiovascular disease; diabetes mellitus; hypothyroidism; GCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antibacterial; antivizal, antifungal, antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                               5.
                                                                                    DB 22; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders,
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ORFX ORF2454 polypeptide sequence SEQ ID NO:4908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating e.g. cancers, proliferative disordeneurodegenerative disorders and cardiovascular disease
                                                                                                                             18;
                                                                                                                                                                                                  18 PVSTRSQHTQPTP--EPSTAPSTSFLLPMGPSPPAEGST 54
                                                                   18.5%; Sco. 35.9%; Pred. No. 55, Mismatches
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                                                                                                                                                                                                                                                                                                                        AAB42690 standard; Protein; 55
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis; contraceptive.
                                                                                                      Local Similarity 35.99 les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-602362/57.
N-PSDB; AAC76899.
                    52 AA
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05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2000;
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                    Sequence
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                                                                                    Query Match
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Matches
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the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, osteoarthritis, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Cu/Zn superoxide dismutase (SOD) polymer of SOD units of at least 2 SOD monomers covalently coupled, carboxy terminus to amino terminus, to each other by a polypeptide spacer of at least 3 amino acids is claimed. The polymers are of formula (SOD monomer - IgA - SOD monomer - IgA - SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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human immunoglobulin A1; hinge region; antiinflammatory agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superoxidedismutase polymers having extended in vivo life - comprising superoxidedismutase monomers covalently coupled by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 55;
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Pred. No. 65;
1; Mismatches
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/note="Hinge #1"
4..20
/note="IgA1"
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38.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hallewell RA, Mullenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 38.3
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-265657/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide spacers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAN80435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to AAZ638 the ESTS can be used for producing secreted human gene products. The 5' ESTS can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNN. The ESTS are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTS can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be
IgA = a 10-100 amino acid long segment of an immunoglobulin hinge region x=2.4
                                 AAN80435 was used to make pSODCF1SODHA1 encoding bacterial expression spacer-linked human SOD monomers. AAN80435 encodes human IgAl hinge region beginning at AA residue 226 to avoid the Cys 225 residue with BamHI and NocI sites at its ends. The SOD polymers have an extended circulatory life and retain the activity of SOD. The cloning and sequencing of human SOD (hSOD) cDNA and prodn. of hSOD in bacteria and yeast are described in EP-138111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                                                                                                                                                                   4;
                                                                                                                                                                           9; Length 21;
                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Human 5' EST related polypeptide SEQ ID NO:1450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giordano J;
                                                                                                                                                                         Score 54; DB 9
Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A,
                                                                                                                                                                                                                                                                                                             AAY65289 standard; Protein; 36 AA
                                                                                                                                                                                                                          15 LPQPVSTRSQHTQPTPEPSTAPSTS 39
                                                                                                                                                                                                                                        Claim 3; Page 788; 837pp; English
                                                                                                                                                                           18.2%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-IB00712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0057719.
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                         Query Match 18.2
Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038446/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ42903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                     AAY65289;
                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                  AAY65289
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                        insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins, have therapeutic value, and the identification of new secreted proteins is valuable. Az42249 to Az42264 and Az464644 to Az464650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide comprises a Humicola insolens family 45 cellulase glycosylated linker used in a novel hybrid enzyme between the cellulose binding domain (CBD) of Myceliophthora thermophila cellulase and Humicola lanuginosa lipase (Lipolase). DNA expressing the linker was obtained by PCR (see AA790506-07). A Construct encoding CBD-glycosylated linker-Lipolase is given in AA770700. A claimed process for desizing cellulose-containing fabric or textile involves treating the fabric or textile involves treating the fabric or textile with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic enzyme linked to a CBD. The process gives improved enzyme performance by modifying the enzyme so as to increase its affinity for cellulosic
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desizing cellulose-containing fabric or textile using an enzyme hybrid - which comprises a catalytically active amino acid sequence of a non-cellulolytic enzyme linked to an amino acid sequence
used for directing extracellular secretion of a polypeptide or the
                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desizing; cellulose; fabric; enzyme hybrid; cellulase;
Myceliophthora thermophila; cellulose binding domain; lipase;
                                                                                                                                                                                                                                                                                                                                   DB 21; Length 36; 48;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. insolens family 45 cellulase linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                   Score 54;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising a cellulose binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vind J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipolase; Humicola insolens; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 43; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 PTPEPSTAPSTSFLLPMGP--SPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 pspapslappslflslppslspp 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW26641 standard; Peptide; 37
                                                                                                                                                                                                                                                                                                                            18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rasmussen MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-DK00041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96DK-0000093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-402610/37.
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                            36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09728256-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bjornvad .ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW26641;
                                                                                                                                                                                                                                                  Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fabric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AAW26641
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                           Zhang S;
                     Mucin peptide MUC1-5
                                                                                                                                                                                                            WPI; 1997-480158/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       50 AA;
                                                                                                                                                                                           Livingston PO,
                                                                                              WO9734921-A1
                                                                                                                                    20-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9734921-A1
  02-APR-1998
                                                                                                                                                    20-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1997.
                                                                                                                 25-SEP-1997
                                                                                                                                                                                                                                                             haemocyanin
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                            Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW31697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia
                                      MUC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                               IgA is secreted by adults at high concentrations in their secretions. However newborn children have no mucosal IgA of their own. Human milk is very rich in IgA providing the infant with passive immunity by coating the mucous membranes with the antibody. Some bacteria secrete IgA proteases which inactivate the infants IgA, when it starts producing it, by cleavage at the hinge region, leading to infection of the infant. The most common allotype of IgA2 has the hinge region deleted and is therefore resistant to degradation by bacterial proteases. See also AAR37993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                      Gaps
                                                                                                                                                                               Heavy chain; hinge region; human; IgAl; IgA; secretion; adult; IgA2;
                                                                                                                                                                                         newborn; children; milk; infant; passive; immunity; mucous membrane;
antibody; bacteria; IgA protease; allotype; resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the heavy chain hinge region of human IgAl
                                                                                                                                                                                                                                                                                                                                                                        Infant formula contg. an IgA protease inhibitor - for providing protection against IgA protease-producing pathogens
                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
Score 53.5; DB 18;
Pred. No. 55;
; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                     13 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA 50
                                                  Score 52.5; D
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pvs----tpptpspstppt-----psp 19
                                                                                                                                                                                                                                                                                                                   (NEWE-) NEW ENGLAND MED CENT HOSPITALS.
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 17; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW35739 standard; peptide; 50 AA.
                                                                                                     AAR37992 standard; peptide; 21 AA
                                                                                                                                                             Heavy chain hinge region of IgAl.
                   7:
18.0%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.78;
                                                                                                                                                                                                                                                                             92WO-US10432
                                                                                                                                                                                                                                                                                               91US-0802338
                                                                                                                                           (first entry)
                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-196741/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
                                                                                                                                                                                                                                                                            03-DEC-1992;
                                                                                                                                           13-0CT-1993
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                               04-DEC-1991;
                                                                                                                                                                                                                                       WO9310818-A.
                                                                                                                                                                                                                                                          10-JUN-1993
Query Match
Best Local 3
                                                                                                                        AAR37992;
                                                                                                                                                                                                                                                                                                                                     Plaut AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW35739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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                   Matches
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ID AAW3
XX
AC AAW3
XX
                                                                                   RESULT 1
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This mucin peptide is used in a vaccine capable of producing an immune response which recognises a mucin. The mucin peptide is selected from MUCI peptide group. The vaccine comprises an amount of the mucin peptide conjugated to an immunogenic protein effective to stimulate or enhance immune response in the subject, together with an adjuvant and a vehicle. The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its derivative. The vaccine can be used to induce an immune response in patients suffering from a cancer of the type where the cancer cells have mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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WUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer;
immunogenic protein; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer; immunogenic protein; immune response; conjugate.
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31.5%;
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This mucin peptide is used in a vaccine capable of producing an immune response which recognises a mucin. The mucin peptide is selected from MUCI peptide group. The vaccine comprises an amount of the mucin peptide conjudated to an immunogenic protein effective to stimulate or enhance immune response in the subject, together with an adjuvant and a vehicle. A cystein is added to the N-terminal of this peptide to facilitate the conjugation with protein carriers. The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its derivative. The vaccine can be used to induce an immune response in patients suffering from a cancer of the type where the cancer cells have mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer, colon cancer or pancreas cancer.
                                                                                                                                                                                                                         Vaccine effective against cancer of the breast, prostate, colon, lung or pancreas - comprising mucin peptide, especially MUC1, conjugated to immunogenic protein, especially keyhole limpet
                                                                                                  (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 11; 45pp; English.
                   97WO-US04493.
                                                         96US-0013775
                                                                                                                                          Zhang S;
                                                                                                                                                                                   WPI; 1997-480158/44.
                                                                                                                                          Livingston PO,
                 20-MAR-1997;
                                                         20-MAR-1996;
                                                                                                                                                                                                                                                                                       haemocyanin
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Sequence

Gaps 18; Indels 13; Score 51.5; DB 18; Length 51; Pred. No. 1.2e+02; 6; Mismatches 18; Indels 13 17.3%; 31.5%; Query Match 17.3° Best Local Similarity 31.5° Matches 17; Conservative

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Search completed: July 13, 2001, 17:44:30 Job time: 172 sec

		Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
	Description	Sequence 56,			Sequence 58,													Sequence 54,					-	-	-	-	-	Sequence 39,
SUMMARIES	QI .	US-08-221-583-56	PCT-US95-04018-56	US-08-221-583-58	PCT-US95-04018-58	US-08-221-583-57	US-08-221-583-62	PCT-US95-04018-57	PCT-US95-04018-62	US-08-221-583-55	US-08-221-583-59	PCT-US95-04018-55	PCT-US95-04018-59	US-08-221-583-61	PCT-US95-04018-61	US-08-221-583-60	PCT-US95-04018-60	US-08-221-583-54	PCT-US95-04018-54	US-08-361-920-19	US-08-479-939-19	US-08-483-432-19	US-08-471-780C-44	-08	US-08-471-282A-44	US-08-466-710C-44	US-08-468-739C-44	US-08-856-074A-39
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	Length	15	15	15	15	15	15	12	15	15	12	15	15	15	15	15	15	12	15	45	45	45	24	54	54	54	54	46
dР	Query	27.9	27.9	27.6	27.6	27.3	27.3	27.3	27.3	26.9	26.9	26.9	26.9	26.6	26.6	26.3	26.3	21.5	21.5	19.9	19.9	19.9	19.5	19.5	19.5	19.5	19.5	18.5
	Score	83	83	82	82	81	81	81	81	80	80	80	80	79	79	78	78	64	64	29	59	29	28	28	28	28	28	22
	Result No.	н	7	9	4	5	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Patent No. 5171685	Patent No. 5518916	Sequence 37, Appl	Sequence 29, Appl	1, A	Sequence 43, Appl	Sequence 43, Appl	Patent No. 5422248			Sequence 15, Appl		Sequence 1, Appl1	Sequence 7, Appl1	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 47, Appl	
_	48 6 5518916-7					ო	ø	-	'n	Н	-	0 1 US-08-099-354-1	~					
55 18.5	29 55 18.5 41	53.5 18.0	53.5 18.0	52.5 17.7	52.5 17.7	52.5 17.7	50.5 17.0	50 16.8	50 16.8	50 16.8	49.5 16.7	49.5 16.7	49.5 16.7	49.5 16.7	49.5 16.7	49.5 16.7	49 16.5	

## ALIGNMENTS

RESULT

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Gaps
                                                                         APPLICATION CONTROLL OF CONTROLL OF THE OF INVENTION: Tumor Necrosis Factor Inhibitors
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
ON ENGRESSES: 62
ADRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
COUNTRY: USA
ZIP: 19403
COMPTTER FRADABLE FORM:
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                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
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100.0%; Pred. No. 0.0033;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
               Sequence 56, Application US/08221583; Patent No. 5486595; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 15; Conservative
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US-08-221-583-56
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RESULT

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ZIP: 19403

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Necrosis Factor Inhibitors: 76
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
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FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4

GET-0595-04018-58

Sequence 58, Application PC/TUS9504018

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.55,
100.08; Pre-
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Heavner, George A. APPLICANT: Kruszynski, Marian APPLICANT: Mervic, Miljenko APPLICANT: Weber, Robert W. TITLE OF INVENTION: Tumor Neci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SQHTQPTPEPSTAPS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 71 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.9%; Score 83; DB 5; Length 15; 100.0%; Pred. No. 0.0033;
                                                               APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
                                                                                                                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                             STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SCETWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
    Sequence 56, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 58, Application US/08221583 Patent No. 5486595 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.5
100.08; F1.
0;
                                               Heavner, George A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                19403
                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-04018-56
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Gaps
                                                                                                              APPLICANT: Heavner, George A. TITLE OF INVESTIGATION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 81; DB 1; Length 15; 100.0%; Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Meber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application PC/TUS9504018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                              ; Sequence 62, Application US/08221583; Patent No. 5486595; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.5
100.08; Pr.
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-221-583-62
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                 STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-04018-57
                          US-08-221-583-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Ponsylvania
COUNTRY: USA
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IP. 19403

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                               27.6%; Score 82; DB 5; Length 15; 100.0%; Pred. No. 0.0041; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 81; DB 1; Length 15; 100.0%; Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 0.0 0; Mismatches
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/08221583 Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEFONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACFERISTICS:
LENGTH: 15 amino acids
                                            REFERENCE/DOCKET NUMBER: CCOF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               Query Match 27.6'
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
                                                                                                                                                                                                                                      MOLECULE TYPE: peptide PCT-US95-04018-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-221-583-57
                                                                                                                                                                                                                                                                                                                                                                                                                   23 SQHTQPTPEPSTAPS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SQHTQPTPEPSTAPS 15
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeLuca, Mark
                                                                                                                                                                                                     amino acid
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US-08-221-583-57
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CURRENT APPLICATION DATA

us-09-800-909-2\_copy\_202\_257.rai

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NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19403
ZIP: 19403
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-221-583-55
Sequence 55, Application US/08221583
Sequence 55, Application US/082
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100.0%; Pred. No. 0.0067;
iive 0; Mismatches 0;
                                                                                                   CCOR-0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.55
100.0%; P1.
                                               REGISTRATION NUMBER: 33,229
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR.
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGIESTRATION UNUABER: 33,229
REFERENCE/DOCKET NUMBER: CCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION: NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
PCT-US95-04018-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 APSTSFLLPMGPSPP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APSTSFLLPMGPSPP 15
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                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 81; DB 5; Length 15; 100.0%; Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Kruszynski, Mijenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Nooris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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CITY: Philadelphia
STATE: Pennsylvania
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATE: US 08/221,583
FILING DATE: 01-APR-1994
FILING PATE: 01-APR-1994
PCT/US95/04018
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                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEC ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 15 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide PCT-US95-04018-57
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COUNTRY: USA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19403
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CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
PCT-US95-04018-59
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                                                                                             GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: GEORGESCHESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STREET: Pennsylvania
COUNTRY: USA
ZIP: 19403
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: TIMOR NOCROSIS Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCOR-0185
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                          Sequence 59, Application US/08221583 Patent No. 5486595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-221-583-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 TOPTPEPSTAPSTSF 40
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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PCT-US95-04018-55
                                     US-08-221-583-59
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Scc...
100.0%; Pred. No. v...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INCORMATION:
NAME: DELUCA MARK
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A. APPLICANT: Heavner, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Fa NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
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FILING DATE: 01-Ac.,
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
APPLICATION NUMBER: 01-APR-1994
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APPLICATION NUMBER: US 08/221,581
                                                                                                                                                                                                                                                                                                                    TELEPANE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 55: SEGUENCE CHARACTERISTICS: LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.9
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US95-04018-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAVHLPQPVSTRSQH 15
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19403
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: G.
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         Score 80; DB 5; Length 15, Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
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                                                                    CCOR-0232
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                                                                                                                                                                                                                                                                            26.9%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCORTELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/08221583
Patent No. 5486595
                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: CCOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENTH: 15 amino acids
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 amino acids
                                                                                                                                                                                                                                                                                          Query Match 26.9
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                     TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04018-59
                                                                                                                                                                                                                                                                                                                                                             26 TQPTPEPSTAPSTSF 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Liberty
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                           amino acid
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US-08-221-583-61
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Gaps
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Fatent No. 5486595
GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                        Tumor Necrosis Factor Inhibitors 76
                        APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitor
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Noris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.6%; Score 79; DB 5; I
100.0%; Pred. No. 0.0086;
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                                                                                                                                                                                                                                    STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US95/04018
; Sequence 61, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.00,
100.08; Pie
                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide PCT-US95-04018-61
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                                                                                                                                                                                                                                                                                   STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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1 PSTAPSTSFLLPMGP 15

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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
21P: 19403
21P: 19403
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTAME: PatentIn Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION NUMBER: 33,229
FILING DATE: Deluca, Mark
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid
TYPE: amino acid
TOPECULE TYPE: Peptide
US-08-221-583-60
```

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Gaps

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26.3%; Score 78; DB 1; Length 15; 100.0%; Pred. No. 0.011; .ive 0; Mismatches 0; Indels

Query Match 26.3 Best Local Similarity 100. Matches 15; Conservative

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Search completed: July 13, 2001, 17:44:49 Job time: 141 sec